

## APPENDIX A: DNA SEQUENCES

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>RXA00212  
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>RXA00214  
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>RXA00313-upstream  
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>RXA00313  
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>RXA00341  
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>RXA00361  
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>RXA00407

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>RXA00414-upstream

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>RXA00414

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>RXA00415-upstream

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>RXA00415

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>RXA00460

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>RXA00538

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>RXA00542

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>RXA00543-upstream

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>RXA00543

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>RXA00544-upstream

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>RXA00544

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>RXA01280-downstream  
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>RXA01286  
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>RXA01286-downstream  
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>RXA01287-upstream  
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>RXA01287  
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>RXA01287-downstream  
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>RXA01334-upstream  
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>RXA01334  
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>RXA01335-upstream  
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>RXA01335  
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>RXA01343  
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>RXA01353-upstream  
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>RXA01353  
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>RXA01356  
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>RXA01363-upstream  
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>RXA01363  
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>RXA01374-upstream

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>RXA01374

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>RXA01423-upstream

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>RXA01423

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>RXA01423-downstream

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>RXA01424-upstream

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>RXA01424

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>RXA01424-downstream

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>RXA01453-upstream

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>RXA01453

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>RXA01453-downstream

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>RXA01480-upstream

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>RXA01480

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>RXA01481-upstream

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>RXA01481

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>RXA01487  
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>RXA01581-upstream  
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>RXA01581  
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>RXA01797-downstream  
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>RXA01824-upstream  
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>RXA01824  
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>RXA01832  
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>RXA01866-upstream  
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>RXA01866  
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>RXA01867  
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>RXA01876  
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>RXA01912  
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>RXA01948  
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>RXA01949-upstream  
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>RXA01949  
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>RXA01950-upstream  
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>RXA01950  
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>RXA02037  
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>RXA02038-upstream  
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>RXA02038  
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>RXA02041  
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>RXA02042  
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>RXA02043-upstream  
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>RXA02043

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>RXA02077-upstream

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>RXA02077

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>RXA02077-downstream

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>RXA02145-upstream

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>RXA02145

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>RXA02179-upstream

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>RXA02179

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>RXA02190-upstream

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>RXA02190

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>RXA02389  
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>RXA02420-upstream

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>RXA02522

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>RXA02522-downstream

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>RXA02533-upstream

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>RXA02615-upstream

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>RXA02633-upstream

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>RXA02633

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>RXN00103-downstream  
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>RXN00163-upstream  
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>RXN00163  
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>RXN00414

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>RXN00414-downstream

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>RXN00460-upstream

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>RXN00460-downstream

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>RXN00542-upstream

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>RXN00542

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>RXN00545

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>RXN00562  
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>RXN00625  
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>RXN00724-upstream

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CACGGTGTTCCACGTCGTATGAACATTGGTCAGGTTCTTGAGACCCACCTTGGCTGGCTG  
GCATCTGCTGGTTGGTCCGTGGATCCTGAAGATCCTGAGAACGCTGAGCTCGTCAAGACT  
CTGCCTGCAGACCTCCTCGAGGTTCTTGCTGGTTCTTGACTGCAACTCCTGTGTTTCGAC  
GGTGCGTCAAACGAAGAGCTCGCAGGCCTGCTCGCTAATTCACGTCCAAACCGCGACGGC  
GACGTCATGGTTAACGCGGATGGTAAAGCAACGCTTATCGACGGTCGCTCCGGTGAGCCT  
TACCCGTACCCGGTTTCCATCGGCTACATGTACATGCTGAAGCTGCACCACCTCGTTGAC  
GAGAAGATCCACGCACGTTCCACTGGTCTTACTCCATGATTACCCAGCAGCCACTGGGT  
GGTAAAGCACAGTTTCGGTGACAGCGTTTCGGCGAAATGGAGGTGTGGGCAATGCAGGCA  
TACGGCGCTGCCTACACACTTCAGGAGCTGCTGNCCA

## APPENDIX B: AMINO ACID SEQUENCES

> RXA00050 (1-2196, translated) 732 residues  
 MSNTENVNGD VEQPNNVISS ESQETPQGDS ASADFALETP TNTVEDAPAS EGSEIEITRVA  
 DTSEDADSAD ADNASNIVINE NEDSSEGANQ PSNESSSTEAL KSGFDALGLP ERVLDVAVRKV  
 GYETPSPIQA QTIPILMEGQ DVVGLAQTGT GKTAALFALPI LARIDKSVRS PQALVLAPTR  
 ELALQVADSF QSFADHVGGI NVLPYIGGQA YGIQLSGLRR GAHIVVGTPG RIIDHLEKGS  
 LDISGLRFLV LDEADEMLNM GFQEDVERIL EDTPDEKQVA LFSATMPNGI RRLSKQYLNN  
 PAEITVKSET RTNTNITQRF LNVHRNKMD ALTRILEVTE FEAMIMFVRT KHETEEVAEK  
 LRARGFSAAA INGDIQAQR ERTVDQLKDG RLDILVATDV AARGLDVERI SHVLNFDIPN  
 DTESYVHRIG RTGRAGRTGE AILFVTPRER RMLRSIERAT NAPLHEMELP TVDQVNDFRK  
 VKFADSITKS LEDKQMDLFR TLVKEYSQAN DVPLEDIAAA LATQAQSGDF LLKELPPERR  
 ERNDRRRDRD FDDRGGGRGD RDRGDRGDRG SRFDRDDENL ATYRLAVGKR QHIRPGAIVG  
 ALANEGGLNS KDFGRITIAA DHTLVLEPKD LPQSVLDNLR DTRISGQLIN IERDSGGRPP  
 RRFERDDRGG RGGFRGDRDD RGGGRDRDD RGSRGGRGG RDRDDRGGG GFRGRDDRGG  
 RGGRGGRGG RD

> RXA00060 (1-2457, translated) 819 residues  
 VTEKTDQTLN LIDGHSMAFR AFFALPAENF STSGGQATNA VYGFLSMLST LLKDEQPTHV  
 AVAFDVGRKT FRTDMFPAYK AQREATPPEF KGQVEILKEV LSTLGITTIE KIDFEADDVI  
 ATLSVAAPKL GFKTILVTGD RDSFQLVNDT TTVLYPMKGV SVLHRTPEA VEEKYGLTPR  
 QYPEFAALRG DPSDNLPNIP GVGEKTATKW IAQYETLDNL LDHADEIKGK VGASLRERIE  
 QVRMNRKLTE MVKDLELPLG PDDFEMKPVQ VAEVAAKFDD LEFGTNLRER VLAVVKAEGS  
 AAPVEEVEAE QVVVDTSQA QWLPARAGQA LALALAGVAK PAAGDTYALA IADTKRHAHL  
 VDVAIDSAED EKALATWLAS EDPKMLHGAK AAYHMLAGRG FELHGVVHDT AIAAYLLRPG  
 QRTYELADVY QRHLQRLST NDNGGQLTLL DAADDQSLVD DVIAILELSE ELTKQLQEIQ  
 AFELYHDLEI PLSGILARME AIGIAVDVAT LEEQLKTFIG QVAQEEEAAR ELAEDPTLNL  
 SSPKQLQVVL FETFGMPKTK KTKTGYSTAA AEIEALAIKN PHPFLDHLLA HRQYQKMKTT  
 LEGLIREVAP DGRIHTTFNQ TVASTGRLSS TDPNLQNIPI RTEAGRKIRS GFVVGEGYET  
 LLTADYSQIE MRVMAHLSQD PGLIEAYREG EDLHNYVGSK VFNVPIDGVT PELRRQVKAM  
 SYGLVYGLSA FGLSQQLSIP AGEAKQIMES YFERFGGVQR YLREIVEEAR KAGYTETLFG  
 RRRYLPELTS DNRVARENAE RAALNAPIRE LPQTSSRP

> RXA00061 (1-210, translated) 70 residues  
 MIRVDRSLKE AAVKSRVLLQ VHDELVEVA AGELEQVREI LEREMDNAIK LSVPLEVSAG  
 DGVNWDAAAH

> RXA00066 (1-813, translated) 271 residues  
 VTDPLSAALD SGRINHAYLF SGPRGCGKTS SARILARSLN CVEGPTSTPC GVCNSCVALA  
 PGGPGTLDVT ELDAASNNGV DDMRELREAR NYAPAESRYR VFIIDEAHMI STQGFNALLK  
 IVEEPPAHLI FIFATTEPDK MIGTIRSRTY NYPFRLLTPG DMRKVLKNAV DGEGVHVDDS  
 VYPLVIRAGG GSPRDSLSIL DQLIAGSGPE GLTYERALPL LGVTSFTLID DSIHALASKD  
 NASMFTTIDN VIEEGLEPRR FTIDLPSDPL R

> RXA00095 (1-2289, translated) 763 residues  
 MNTSPFTPGS PDLIDGLNEQ QRAAVEHIGS PLLIVAGAGS GKTAVLTRRI AYLMRYRGVH  
 PQQILAITFT NKAAAEMRER VSQLVGPVAF RMWVATFHSV CVRILRQQAQ LVEGLNTNFT  
 IYDSDSRRL LTMIAKDLEL DIKKFSARTL LGAISNLKNE LVTPQALAD AERTNPNYET  
 VVARAFSEYQ SRLRRANAVD FDDLIGETVR IFREHPPVAE YYRRFRHVL IDEYQDTNHA  
 QYELISTLVG KPDQDPSELC VVGDSQSIY AFRGATIRNI EEFERDFSNA RTILLEQNYR  
 STQTILSAAN AVISQENRR PKNLWTALGE GEQIIGYVAD NEHDEARFIA SEIDNLVDHG  
 MSYSDIAIMY RTNNSSRALE DVFMRGTGVPY KVVGGTKFYE RKEIRDIIAY LRVLENPDDT  
 VNLRRRIINTP KRGIGDRAQA FIALHSENNQ ISFGQALLDA ALGKVDLLGA RGKNAAIKFN  
 ELFDALRSEL PTMVNEVTGL PDIGQVISRI LDITGYKAEL EASNDPQDGA RLDNLNELVS  
 VAREFSSDAA NRMVNEVPEG EAQPGSLQAF LERVSLVADA DQIPDSNGV VTLMTLHTAK  
 GLEFPVIFLT GWEDGQFPHL RSLGDAKELA EERRLAYVGI TRARKRLYMT RAMLRSSWGN  
 PVTNPPSRFL QEVPAELIDW RREEPQMSSA WAPRPTRSIP TKTRTNKQL DLSVGDRVNH  
 DKYGLGTVLS SDGSGPRATV TIDFGSSGKV RLMLLGGVPM EKL

> RXA00103 (1-4560, translated) 1520 residues  
 MAKSIILSRFR PQVAEWFDRV FASPTPVQEG TWEAVSKGKN ALVVAPTGGG KTLAAFLWAL

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DSLTEQTGQQ VLDTGTPVPV RGGKVKVLYI SPLKALGVDV ENNLRAPLTG IARTASRMGL
DVPNITVAVR SGGTTPSAERA RQVRKPAHIL ITTPESAYLM LTSKAGATLS DVDVVIIDEI
HAMAGTKRGV HLAALTLELLE KLVGRPVQRV GLSATVRPLE TVAGFLGGGR PVEIVAPPAE
KKWDLTVTVF VEDMSDLFVQ EPGSTIGELV MDDPLGITGE SALPTQGSIW PHIEQQVYNQ
VMSAKSTIVF VNSRRSAERL TSRLNEIWAM EHDPELSLPQ LRRDPAQIMS SADVAGKAPQ
VIARAHHGSV SKDERATTET MLKEGRRLAV ISTSSLELGI DMGAVDLVIQ VESPPSVASG
LQRVGRAGHT VGATSIGSFY PKHRSDLVQT AVTVQRMKEG LIEEIHVPKN ALDVLAAQQT
AAVSIKDVQV DEWYETIRKA YPYRDLAREV FDSVIDLVSG VYPSTDFael KPRVVYDRVS
GVLEGRPGSQ RAVVTSGGTI PDRGMFGVFL VGDGPRRVGE LDEEMVYESR VGDVFTLGAS
SWRIEEITRD QVLVTPAPGH TGRLPFWTGD AAGRPAELGK ALGAFRRSTL TDPSSSGLEG
WAHDNLIAFL QEQEESTGVL PDEKTLVLER FKDELGDWRI VLHTPYGRGV NAAWALAVGA
KIAEETGMDA QAVAGDDGIV LRLPEGDEDP SAALFMFEAE EIETLVTEQV GNSALFASRF
RECAARALLL PRRNPGKRAP LWQQRQRAAQ LLDVARKYPS FPIILETVRE CLQDVYDLPA
LKNLIEDLQL RKVRIAEVTT QQPSPFASAL LFNYTGAFMY EGDSPLAEKR AAALALDPAL
LAKLLGEVEL RQLLDPDIIA EVHQQLRRQG DRAARNNEEL ADSLRILGPI PLDELGEHIT
FENPDLEDRA MTVRINGREH LAQVLDAPLL RDALGVPVPP GVPAQVETIT DALEQLVNRW
VRTRGPFTAN DLAEAFGLGI ATAITALQSA PVIEGRYRQG VDVQEYCATE VLSIIRRRSL
AAARKQTRPV SQSAFARFLL DWQQIAPVGA TPELRGVDGT YTVIEQLAGV RLPASAWEDL
VLPRRVADYS PIHLDELTSN GEVLIVGAGQ AGSRDPWISL LPVDYAAQLV GEASTSMSPL
QDAVLDQLRA GGAFLFSDIL EENFGYTAAQ LQEA MWGLVE AGLVSPDSFA PIRARLASGT
TAHRAKRRPA RSRLRTRTSF ASDVPPDMRG RWTL SVQPAD ATSR SVAHGE GWLD RYGVLT
RGSVVAEDIV GGFALAYKVL SGFEESGKAM RGYFIEGLGA AQFSTPAID RLRGHDDSPD
VEGWVSGATD PDVYLIAAAD PANPYGAALP WPEQGPSRAA GAMVVLCDGL LLAHLTRGGR
TLTVFSDNIP KIATALITYE RLTVEKINGD NVFDSPLLEQ FRKHGATITP KGMFRFRPPVA
RETPSDTLPT RTFRGGFGRR

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> RXA00157 (1-1263, translated) 421 residues
ARIVAEQREA EAVEKKVQTE AAIAANSEQL NVLTTNRSTL VAQRDGAERN LAIARAQADN
LQQQRAEYEE FQQAQEQARIQ AEAEAQAAAE EKRRADEAAA QAAAEAEQAAA QQAQAAEEAQ
AAQAAETAQA QAAQAAETQA AQAAQAQAEA NDRAAAQORA AEQAQAAEQQA QREADAQAAN
DAQAALREQ ALTAASIAAA ALIAASQSSH ATTQNPYPTD EDADPTDIAD IQGPTQPGTG
ESGDSQSNSS DNDSTGNDST GSDSSDSOSS GNDSSSEVISG DRSAQIETVI ARAMSQLGVO
YAWGGGNANG PTLGIRDGGV ADSYGDYNKV GFDCSGLTLY AFAGVGISLP HYTGYYQHG
TKVSPSEMQR GDLIFYGPGA SQHVAIYLG DQMIEAPNSG SVVKISPVRW SGMTE SVVRL
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> RXA00163 (1-561, translated) 187 residues
LDQAGLDSVE LLALRDVEAY DEPIEDGRFT ADNAQIKARA GVTHGTGIATI ADDSGIAVEE
LNGMPGVLSA RWSGAHGNDT ANNELLLAQM EHVDPERRNA AFVSVCVLAL PDGQEFVQEG
RWEGQLLRGP KGENGFYDYP LFIPAEIDG QGRSSAELSA EEKDALSHRG QALRGLVEKI
AQVAAAS

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> RXA00208 (1-849, translated) 283 residues
MNTAPAPRRR EMKIKTATVT GVRQISPOLI RFSFDCPEIV GADLGFTDHY IKILFVPAGA
DYSWPFDMAE IAETQPRELQ PVRRTYTFRT VDTVAGTFDI DFVAHGTDGL AGPWAQQAQV
GDVIAFGGPG GAWKPETTYE HYVLAGEDEA APAIFAALH LPAGTTAKAF IEISSNEARF
NAPASDNIEV VWVPRDGATH GTLLIDALRQ DGYPTKKT SW FIHGVAEMVK ETRKFLFVEG
NVDKADASIS GYWR LGMTED QWQASKREFN EQNEAEELAL SKA

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> RXA00212 (1-1560, translated) 520 residues
MNILCLLCWK FAVRCSSLWR ISQEVNAQRI ADGGKPFANP RNAAAGSLRQ KNIEDVKKRR
LRMISHGIGF TEGFSPASQH DAYLALAAWG LPTSPYTEAV TDPEDVVKV SYWADHRHDA
LHEMDGLVIK VDDIASQRAL GSTSRAPRWA IAYKYPPEEV TTKLLDIQVG VGRTRGVTPF
AVMEPVLVAG STVSMATLHN QSEVKRKGVL IGDTVVIRKA GEVIPEVLGP VVELRDGTER
EYIFPTLCPE CGTRLAPAKA DDVDWRCPNM QSCPGQLSTR LTYLAGRGAF DIEALGEKGA
EDLIRTGILL DESGLFDL TE DLLSSNVYT TNAGKVNASG KKLLDNLQKS KQTDLWRVLV
ALSIRHVGPT AARALAGRYH SIQALIDAPL EELSETDGVG TIIAQSFKDW FEVDWHKAIV
DKWAAAGVTM EEEVGEVAEQ TLEGLTIVVT GGLEGFTRDS VKEAII SRGG KASGSVSKKT
DYVVIGENAG SKATKAELG LRILDEAGFV RLLNTGSADE

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> RXA00213 (1-573, translated) 191 residues

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VTEDNAQLRR TWNDLAEKVR YHRDRYYNEQ PEIPDADFDA LFKQLQQLEE DHP ELAVPDS  
PTMVVGAPVA EQSSFDNVEH LERMLSLDNV FDEQELRDWL GRTPAKQYLT ELKIDGLSID  
LVYRNGQLER AATRGDGRVG EDITANARVI EDIPHQLQGT DEYPVPAVLE IRGEVFITVE  
DFPGGQRAAH C

> RXA00214 (1-711, translated) 237 residues  
MNSPSNPSPT VPSLDTTKML SFDLETTGVN PFDTRIVTSA MVTITSKGAE PIELLADPGI  
EIEPAATAVH GITTEHARAN GRPHDEVLA E TISRLRAGWQ AGLSVIVFNA SYDLTVLRNH  
DPSFTIDGLV YDPFVIDKVK DRYRK GKRTL TDMCAHYDVQ LGNAHEATSD ALAAARIAWK  
QVRLWPELTK MTGEELMEFQ AVNYEQQKS FRSYLIGQGR DASDVNTSWP VQTD PAS

> RXA00313 (1-939, translated) 313 residues  
MAGNDSRRGG LRKTNKKGAT KGSGGQVRRG LKGKGPTPKA EDRTYHAAHK RKVERDRRDR  
GRHQREMP EL VVGRNPVLEC LHARVPATAL YVAEGAANDE RLSEAVHTAA GRNLPVLEVN  
KLELDRMTGN GMHQGIGLAI PPYEYADVHD LIANA AASKK PGMFVILDNI TDPNRLGAVI  
RSVGAFGGNG VIIPERRSAS VTAVAWRTSA GTAARVPVAK ETNMTRVVKE FQONGYQVVG  
LDAGGDHTLD TYDGTDNVVI VVGSEKGKIS RLVRENC DTI MSIPTEGWVE SLNASVAAGV  
VLSEFSRQRR IKG

> RXA00341 (1-1407, translated) 469 residues  
MKLYAAVLDF EPVAQEF GVE RGFDPHIHDE AASSVDRYAQ EREDLLHMPF VTIDPVGSRD  
LDQAVLIEEI DSGFRVHYAI ADVAA FVEPG SELEKISLHR GQTIYLPDSP ARLHPEELSE  
DAASLLEGQT RPAVVWSIDL DERGEVTATK VRRGLVKSRA RLDYDQAQID AENGR LHPSI  
SLLPKVGQLR QESALRREAV NLSIPSQRVV KVPND DAGEH YEIVIEPRPH IMDYNSEISL  
LTGMVAGEMM VKAGHLLRT LAPATKESEA TFRSEAQALG FEIAPEQPIG EFLQSVDPNT  
PKGMAIQREA QKLLRGSGYA SVKNGDSEVH SGVGGYYAHV TAPLRLRIDR FATEHCLAIA  
SGTDVPEWVT RVEEQVLDTM KYSSILASQV DNACLDL TEA TVLKYWEGQN FNAV VASEP  
EKNSARLFVY KPPVLAKCIG APEQGTNQDV TLVTANLKKR EVLFAW PAD

> RXA00361 (1-1848, translated) 616 residues  
MTTSETAPSK ASLYELLEGV SLSDERTFRR RLSKARAPKA LGAIKADIDK ARLLIDEKSQ  
LIPSITYPEN LPVSSRRDDI AEAIRDNQVV IIAGETGSGK TTQIPKICLD LGRGRRGLIG  
HTQPRRLAAR TVAERIADEL QDIGESVGY AIRFDDRVS HTSVKLMTDG ILLAEMQRDR  
FLNAYDTIII DEAHERSLNI DFILGYLRQL LPKRPDLKVI ITSATIDPER FAEHFADASG  
KPAPIIEVSG RTFPVEIRYR PLEVLDGDKI IDTDPLDGLC SALEELMAEG DGDILCFFAG  
ERDIRDAMEA IEARRWK GVE VTPLFGRLSN QEQRHVFSPH SGRRIVLSTN IAETSLTVPG  
IHVYVDTGTA RISRYSVRTK VQRLPIENIS QASANQRSGR CGRVADGIAI RLYSEDDFNS  
RPEFTDPEIL RTNLA SVILR MASLRLGDIN DFPFVQAPEQ RSIRDGILL HELGAL TDDT  
QADGSPQLTQ IGKDLANIPV DPRMARM LVE ANT LGCLHSV MVIVSALT IQ DVRERPLEFQ  
AQADQAHARF KDTTSDFLGF LKLWEYIADQ RNQSSGNSFR KQMKKEFLHY MIREWWDLV  
RQLEQIGQQL GWAKKE

> RXA00407 (1-576, translated) 192 residues  
LNVAQVEALA RAGAVDCLGV GRRQALWQAG VAATEKPGML PGLSVIEAPA LPGMSAFELM  
ATNISATGVT ADYQPMALIR ERMEELGIVP ADRLL EVEDG TRLRIAGIVT HRQRPQTASG  
LTFLGMEDET GLNMVMVSVG LWQRQ RVLAR NAKALIIRGI VQNAQGVATV VADRLEPLDM  
GEFLSRGSRD FR

> RXA00414 (1-420, translated) 140 residues  
MQGEASVPFA ELHATSSYNF LTGASDPSDV VVQAKKLGLA ALSVMDR DGF YGAVRFAEAA  
AEAGMHTVYG AELSLQEGVL TVLCKNPEGY KKLSHLISDA KMARGEKGKF AIRRCQWLLN  
MLQGIGWSLQ VFSGWTKSTM

> RXA00415 (1-1962, translated) 654 residues  
MVAEHAAGDW VVLAGFQWLD KIDYVIDCFK PENIVLEFGS TMTPEDADR N EYLRR TQAKF  
QLRGILSTNP ESAARGSVRL AGAKQALARK MPLADA ESEL HPMGTTWMRS GDTLLKAHPD  
YADLIATTVE LAAECAFTLD LVAPNLPKWD TPGEHTEMSW LAHLVSTRID TRYVGRSADI  
KARAATQIDY ELGVIEKLGF PGYFLVVNDL VEFCD RSNIL CQGRGSAANS AVCFVLGITN  
AEPISAGLLF ERLSPDRDG PPDIDIDIES GRREEVIQYV YEKYGRDNAA QVANVITYRT  
KGAMRDAARA LGYPQGAADA WAKGTSEPPD DVLELAAQFK GQPRHLGIHS GGMVICDRPI  
ADVVPVEWAR MDNRSVVQWD KDDCATAGLV KFDLLGLGML EAIHHMLDLV AEHRGKKINL

WELDLAEPEV YDMLCKADAV GVQVESRAQ LSTLPRLKPR TFFDLVVEVA LIRPGPIQGG  
SVHPYLRRRA GEEAITYDHP VLEKSLGKTL GIPLFQEQLM QVAVDAAGFS GGEADSLRRA  
MGSKRSPERM AALRSRFFQG LKDTNGIVGE TAEKLWNKIV AFAAYGFPEHSQSFSALSVY  
FSAWFKYHYP AEFCVGLLRA QPMGFYSQPS LISDARRHGV SILPITVNSD GVEA

> RXA00460 (1-378, translated) 126 residues  
MPEHPLHVIF DNPVIPPNTG NAIRMCAGTG AHLHLVEPLG FELTEKHLRR AGLDYHDLAD  
VTVHATFDEA MAAVPGRVFA FTTTANTRFT DIAFEPGDAL LFGTEPTGLP QEHVEHSRIT  
SELRIL

> RXA00538 (1-1269, translated) 423 residues  
MSRISARTLA IALAGATAAS LAVVPAATAN PAGTAPVINE IYEGGGNSGS LFSNDFIELY  
NPTSGDISLD GWSVTYYAAN GNSGGTTNLT GNIPANGYYL IQQRAGSNNT GALPTPDATG  
NLAMGASQGS VALTDNSGLT ADLVGFGGTS MFEGTAAAPE TSNKLSVQRK EVGADSDNNS  
VDFETGAPTP TSSGGSAPVD PGEPETPVNP GETVSIAQIQ GTGLATPLEG QTVTTEGIVT  
AVYAEAGGFNG YYIQTPGSGT APKVAGDASD GIFVYVGSNG SYPELGASVT VTGKATEHYE  
MTQLGNSSFT VSDTAFEPVT PLELDTVPTG DDIREAYEGM LLKPTGAHTV TNNYATNTFG  
EIALAPGNEP LYQATQMVAP GAEAIAYEAE NVAKQITLDD GRSGNYTRGD SSTPMAWLVO  
DGG

> RXA00542 (1-519, translated) 173 residues  
ALFLTIVNVWR QAAENVAESL SKGMRVIVTG RLKQRSYETR EGKRSVFEV EADEVGPSLT  
FAKADVQRTF RGGNSGGNYG GGNQGGGLGG NQGNQGGGFS NQNSGGFGGN QGNQQQSNQG  
GFGGNQNSQ GNNFNQGGFG GGSPQAAPDN DPWNSAPPAG SGGFGGADDE PPF

> RXA00543 (1-426, translated) 142 residues  
MKLILTAAVE NLGVAGDIVE VKNGYGRNLL LPRGLAIVAT PGAEKQIEGI KRAQEAREIR  
DLDHAREVKV ALEALEGVTI AVRTSESGKL FGSVKTDIV DAVKAAGGPN LDKRAIVLPK  
NLVKTGKYQ VEAKLTDGIV SA

> RXA00544 (1-1530, translated) 510 residues  
MATDTHAASF DDDYVPPQEP SDSFADDAHV DVPAPAFEDF SPAQAFGQGT RGGDSQGFKK  
RGRKDESREY RDRQPPYDN DAEMGVLGAM LLSPTTVIDI LDILTPEDFY RPSHQLIFQA  
IIDLFSNDRD IDPVIIVSGRL DRTNDLDRVG GGAYLHDLIQ SVPTAANARY YAEIVSEKAV  
LRLVDAGTR VVQLGYEGDE GAEIDAVIDR AQQEVFAVSQ KNQSEDYAVL ADILDETMAE  
LEMLNDGGIA TGIPTGFKDL DDLTNGLRGG QMIIVAARPG VGKSTIALDF MRSASIKNNM  
ASVIFSLEMS KSEIVMRLLS AETEIRLADM RGGKMDETAW EKMVQKLDKV AQAPLFIDDS  
ANLTMMEIRS KARKLKQKHD LKMIVVDYLQ LMSSGKRVS RQQEVSEFSR QLKLLAKELD  
VPLIAISQLN RGPESRTDKR PQLADLRESG SLEQDADIVM LLYRPDSQDK DDERAGEADI  
ILAKHRGGPI DTVQVAHQLH YSRFVDMARG

> RXA00545 (1-255, translated) 85 residues  
MIILDPSQDE RTVAPSLDKF LEVVRKDKGD VVKVDVWGKR RLAYPIDKKE EGVYAVVDLK  
CESATVLELD RVLNLNDGVL RTKVL

> RXA00562 (1-630, translated) 210 residues  
MDADPLIEDD VSGAEVKDSS DEPLLALTRY VFDRGERPVT RGLFHQVA AI LSIVSGSVLS  
TYAWMELVWV QALGVMVYAL AMLGLFAVSA AYHRGPWRRL HTVAWWRKAD HSTIAVFIAA  
TYTPLCLIVL EPGTAAWMLG IAWVGAIDSV IMNMVWINHP RWLSVLVYLA LGWLIVPLVP  
QLWSGAGPTV VWLLLAEGIV YSVGALVYGF

> RXA00625 (1-339, translated) 113 residues  
SDHDIKVG F NLSETTEPTI PVEPTDPAEP TDPTTPVKPT DPVETTDPS E PTDPAEPTDP  
AEPTDPEETK KPEEPKNPGS SNGSSQYATI AAIIAAILGA IALAFQFFHS SSN

> RXA00670 (1-489, translated) 163 residues  
MPTPKKGARL GGSASHQKKI LSNLAASLFE HGAIKTTDAK AKALRPYAEK LITKAKSGSV  
ADRRNVLALV PNKEIVAYLF NELAPKFENR PGGYTRI I KL ENRKGDNAPM SQISLVLEET  
VSAEASRATR ASASKAAEE AETEEVVEAP AEETATEEAA EEK

> RXA00671 (1-1014, translated) 338 residues

MLISQRPTIT EEFVNNARSR FVIEPLEPGF GYTLGNSLRR TLLSSIPGAA VTSVKIDGVL  
 HEFTTISGVK EDVSDIILNI KGLVLSSDS EPVVMQLVKE GPGVVTAGDI QPPAGVEIHN  
 PDLHIATLNE TAKIEIELIV ERGRGYVPAT VTATGGEIGR IPVDQIYSPV LKVSYPKEAT  
 RVEQRTDFDK LVIDVETKNS ITARDALASA GKTLVELFGL ARELNIAAEG IEIGPSPQET  
 EYIAAYSMPI EDLDFSRSY NCLKREDIHT VGELAERAES DLLDIRNFGQ KSINEVKIKL  
 AGLGLTLKDA PEDFDPSTLE GYDAETGGYI DVEAEDSE

> RXA00672 (1-603, translated) 201 residues  
 MARYTGPAIR KSRRLRVDLV GGDMAFERRP YPPGQAGRAR IKESEYLLQL QEKQKARFIY  
 GVMEKQFRRY YAEANRRAGK TGENLVVLE SRLDNVYRA GLANTRRQAR QLVSHGHFTV  
 NGKAIDVPSF RVSQYDIINV REKSQKMNWF EEAQDNLADA VVPAWLQVVP ENLRILVHQL  
 PERAQIDIPL QEQLIVEFYS K

> RXA00673 (1-90, translated) 30 residues  
 LQAAGLEIGS ISDVTPQPHN GCRPPKRRRV

> RXA00694 (1-396, translated) 132 residues  
 MTMTDPIADM LSRVRNASNA HHDTVSMPS KIKANIAEIL KQEGYIANYT VEDAKVGKTL  
 SLELKYSNTR ERSIAGLRRV SKPGLRVYAK STNLPQVLGG LGVAIISTSQ GLLTDRQATE  
 KGVGGEVLAY VW

> RXA00695 (1-534, translated) 178 residues  
 MSRIGKEPIT IPSGVETKID GQLVEVKGPK GTLNVNVPPEP ISVAVEDGKI VVTRPDDHRT  
 NRSLHGLSRS LVNNLVVGVV EGYTIKMEIF GVGVRVALKG KDLEFSLGYS HPVLIASEG  
 ITFAVDGNTK LSVSGIDKQK VGQVAAVIRR LRKDDPYKKG GIRYEGEQIR RKVGKTGK

> RXA00696 (1-402, translated) 134 residues  
 MSNTENKQKR VSVGKDIATR RRVARARRHF RIRKNLRGTP EAPRLVVHRS SRMHVQIID  
 DVAGHTLAAA SSIEAEVRAT EGDKKAKGAK VGQLIAERAK AAGIEQVVFV RAGYKYHGRV  
 AALADAAREG GLKF

> RXA00697 (1-633, translated) 211 residues  
 MPGRERRDGG RSADDNKQND RNERRGGRR DRRNQQQDE RSQYIERVVT INRVSKVVKG  
 GRRFSFTALV IVGDGKGMVG VYGKAKEVP AAIQKGAEAA RKNFFRVPMV NGTITHPVQG  
 EKAAGIVMLK PAAPGTGVIA GGAARPVLEC AGIQDILSKS LGSDNAINVV HATVDGLKQL  
 VRPEEVAARR GKTIEEVAPA RILRARAGQE A

> RXA00698 (1-183, translated) 61 residues  
 MALKITQIKG TVGTPKPHRE NLRSLGLKRI RHTVIRPDTP EVRGMILAVR HLIVVEEVAG  
 E

> RXA00699 (1-444, translated) 148 residues  
 MSEPIKLHDL RPAAGSNKAK TRVGRGEASK GKTAGRGTKG TKARKQVSAA FEGGQMPLOM  
 RLPKLKGFKN PNKVDYQVVN IADLAEKFPQ GGDVSIADIV AAGLVRKNEL VKVLNGNDIS  
 VKLNVNTANKF SGSAKEKIEA AGGSATVA

> RXA00706 (1-267, translated) 89 residues  
 EFLDRLLTVA LPRIRDFRGL SDQQFDGHN YTFGLTEQTM FYEIDVDKID RPRGMDITV  
 TTAVTDDEGR SLLRELGFPP KGEDGNRQQ

> RXA00709 (1-339, translated) 113 residues  
 VADNTGAREI LCIRVLGGST RRFAGIGDVI VATVKEATPG GNVKSGEIVK AVIVRTKKET  
 RRADGSYISF DENAAVIAIKN DNEPRGTRIF GPVARELREK KFMKIVSLAP EVI

> RXA00710 (1-312, translated) 104 residues  
 MKVHKGDMVL VISGPDKGAK QGVIAAFPKT EKVLVEGVNR IKKHVANSAP ERGAESGGIV  
 TQEAPIHVS VMVIDSDGNP TRVGYRFDEN GKKVRVSRN GKDI

> RXA00711 (1-156, translated) 52 residues  
 MTENYIPRLK TRYQDEIRTK LQGEFEFENV MQIPGVTKIV VNMGVGDAAR DS

> RXA00717 (1-960, translated) 320 residues  
 VTPPARRDGT PDKKQSNRSG GYRSSVRGYK PGSSRPNTRO QPQKKDEILL SNAKPAKKQN  
 VKSDDDDWSMG FLNRNDSQDV RLQKVLAQAG VASRRHAEIL IDQGRVEVND RIVTTQGVVRV  
 DPNNDVIRVD GVRIHINEDL EYFVLNKPGR MHSTMSDELG RPCVGDVSE KTASGQRLFH  
 VGRDLADTEG LLLLTNDGEL ANRLMHPKYE VSKTYLATVR GEATNKLVS LRDGVELEDG  
 PAKADFAQII DVFQGKSLR IEIHEGRKHI VRRFLDELGF PVERLVR TKL HTVQLGDQKP  
 GSLRALNSSE LTSLYKVVQL

> RXA00789 (1-243, translated) 81 residues  
 MTNPDIVGSG QGNDSFEPVA QLSYERARDE LVEIVKILEL GQMGLDESLK YWERGEALAK  
 RCEEHLGAS ARVEQALNQA E

> RXA00790 (1-1026, translated) 342 residues  
 RNRPTPLKDG DRVIVYGKPA FYAGRGTFSL WVTDIRPVGI GELLARIEEL RKRLAAEGLF  
 DPARKKRLPF LPNRVGLITG RGSAAERDVL SVAKDRWPEV QFEVINTAVQ GASAVPEIIE  
 ALRVLDQDPR VDVIIIRAGG GSVEDLLPFS EEALQRAVAA AQTPVVSAG HEPDTPVLND  
 VADLRAATPT DAAKRVVPDV AEERMLINQL RSRSAALRG WVQREQQALA AIRTRPVLDN  
 PMTPINRRRD EIAQAVGLIR RDVTHLVRTE QALVASLRAQ VSALGPSATL ARGYSVVQVI  
 PRDGSAPVV TTIEQSPPGS QLRIRVADGS ITAASMGTOQ AN

> RXA00798 (1-2355, translated) 785 residues  
 DYWDLAEFEN ARENGKADSD NPSSFTARLS TIDGNRVAQG RDFNDRGELT SEAVVVDKQR  
 AGEALAEALG QEMAVVGVEE KPYTRRPYAP FMTSTLQQES GRKLHYTSE TMRIAQRLYE  
 NGHITYMRTD STSLSEQGMK AARDQALELY GA EYVSPSPR TYDRKVKNSQ EAHEAIRPAG  
 ETFATPGQLH GQLDAEEFKL YELIWQRTVA SQMADAKGTS MKVTIGGTAK TGEKTEFNAT  
 GRTLTFFPGFL RAYVETTRTA DGRDVADNAE KRLPLLSEGD LLKVLSEAD GHSTNPPARY  
 TEASLVKKME DLGIGRPSTY ASIIKTIQDR GYVYSRGNAL VPSWVAFVAV GLLEANFTSL  
 VDYDFTSSME DELDNIAAGR EGRTWLNLF YFGDAEADQS MAESVARQGG LKALVDANLE  
 HIDARSVNSL KLFDDAEGRA VNVRVGRYGP YIERIVGTTA EGEPEFQRAN LPEETTPDEL  
 TLEVAEKLFA TPQGGRELGI NPANGRMVVA KEGRFGPYVI EQVTDSEERAG AEAQAEVVA  
 AERKADEQR ATDGMRPKNW ETKTAANQKE KRINQLVEEN LKPATASLFS GMEPAAVTLE  
 EALKLLSLPR EVGVDPDSNE VITAQNGRYG PYLKKGSDSR SLNSEEQIFT VTLDEARRIY  
 AEPKRRGRAA AQPPLKQLGD NDVSGKPMTV KDGFRFGPYVT DGTNNSLRK GDVPESLTDA  
 RANELLSEER AKEAADGGAP AKKTSTKKA AKKTAKKT AKKTVRKAPP KTTKNVVKAG  
 AKKKS

> RXA00807 (1-1119, translated) 373 residues  
 VFDSLGSKT VSKTLFDAAS SARALVRART TERARARAEH QNPAMIHDSG FAQSWLFTGP  
 PGSGRSVAAK VFAATLVCSN PDVVGCGQCE DCRAAMGGSH PDIEHIVPQQ LSIGVDAARE  
 VIKAAVSPV AGNWRVVFIE NADRLTMQAA NALLKTVEEP TESTVMILCA PTTDPRIAI  
 TLRSCRHLI IPTPSIAEVA RILVAEGNVS QADAELAAAA SGAHIGRARY LAHNNAAQRR  
 RASILNLAEL IFHGDVAFRS VNTLVKVMET EAKDSNKEKE EGDLEAVRIS LGMAAKGKGV  
 HKA VRGGAGD FKALEDQQL RRTRFLRDSL DLALVDLAGI YRDAIISSQ AQVGLTHPDM  
 EGLSQELATK VSQ

> RXA00809 (1-510, translated) 170 residues  
 LTPPDFESEK TQAMRPSFGE ELAAIVSKRY SESTLTHMVT LPASKAKYVD WPSWVPASLR  
 DALVNRGINK LFSHQEQTAH LAWNGQHVVV ATGTSSGKSL GYQLPILSAL GTDPTACALY  
 LTPTKALGSD QLTSTSTLLR DIPDFHPIN APYDGDTPSE ARSGIRDLR

> RXA00817 (1-1710, translated) 570 residues  
 FYGSHTPVIL ASATSSDPEI HASRLGAPV KAVTEDGAPT GERTVLLWEP GFIEGAEGEN  
 GAPVRRAAST EAANIMATLI SEGARTLTFV RSRRQAEIVA LRAQEELSTL GRPDFARRVA  
 SYRAGYLAED RRRLERLLDD GTLLGVASTN ALELGIDVGG LDAVVTAGFP GTVASFWQQA  
 GRAGRRGQGS LVVLVARDEP MDTYLVHHPA ALLEKPEVAA VFDPTNPHVI RGHVYCAAVE  
 KPLTEAEVAA FGAQKVVEKL EIEGLLRKRP RGWFAVEKPM SEDPDELSPD SAHQQVSLRG  
 GSGSEFMIVD ITDGRLGTL DSAKAMSQTH PGAVYLHQGE SFVIDELDL ENLALARPEL  
 PDYTTIYASD TDIRITSAPL EDEVFDAGG LWVANVEVQV TDRVTGYVTR LSDGTTLDAT  
 PLYLPPQILQ TRAVAYTIDP LALEAMGIPA ADIPGALHAA EHAAIGMLPL LATCDRWDIG  
 GVSTALHADT GYPTVFVYDG MDGGAGFADT GFRFAQWIE ATFEVVRSCS CESGCPSCVQ  
 SPKCGNGNNP LDKAGAIKLL GAMVTLLGTS

> RXA00823 (1-780, translated) 260 residues  
MGSITPQKR RVGSHIANKG QETDIGRKRR ARRINRTLTV AYPDAHCELD FTNPLELTV  
TILSAQCTDV RVNQVTPALF KRYPTATDYA NADRTELEEF IRPTGFYR NK ATSLIGLGEA  
LISLHDGQVP GTLEQLVELP GVGRKTANVV LGNAFGVPGI TVDTHFGR LV RRLKLTDEED  
PVKVEKVMNE LIEKPEWTMF SHRLIFHGRR ICHSRRACG ACMLAADCP S FGLEGPSDPF  
EAQKLIKSD REHLLKMAGM

> RXA00890 (1-1275, translated) 425 residues  
LSIATVVALL FSGLLGAVES ALSSVSRARV EQMLKDEASG SASLLRVIDE RALHINMLIM  
LRTLLDASAA VFAGAIANV MDSWAWGIVL AIVVVSLLTF AVVGVEGRTV GRKNPYSVML  
RSVVLSGLA KILGPIARGL IWIGNIAPG PGFRNGPYAT EVELREMVDI AQEHGIVEIE  
ERRMIQSVFD LASTTVRQVM VPRPEMIWIE SGKTAGQATA LCVRS GHSRI PVIGENVDDI  
IGIVYLKDLV QKTYATDGG KSVLVDEVMR EATFVPDSKS LDALLQEMQE DHKHIAILVD  
EYGGVAGLIS IEDILEEIVG EIADEYDARE VAPIEKIGDR TYRVVSRLSL EDLKDHIIEE  
LDLEIEFGDE IEDQVDTVGG LIAFELGRVP LPGATVETCG LKLTAE GAKN RRGRLRMHSA  
VVEVG

> RXA00898 (1-789, translated) 263 residues  
MRIVNWNVNS ARTRVDRMVD FLLRHVDV DL AVQETKCKDE QFPTERFTEI GYEV AHFGLN  
QWNGVAIISR VGIENVETHF PAQPGFNKDI TKEQSIEARA IGARCGGVQV WSLYVPNGRE  
IADPHYDYKL RWLFSLRNYV IDTLEYRPEE KLVLLGDFNI APTDIDVWDI AAFEGKTHVT  
EPERAAFDGL IEAGLKETTP GPGTYTYWDY KGARFLKGE G MRIDFQLASP ALAATAGET F  
VDVEERSGTG ASDHAPVIVD YKV

> RXA00967 (1-363, translated) 121 residues  
MPVQDAGERN NND RPVM PGE ILREEFMEPL GLSQNG LARA IGVP PRRINE IVHGKRAITA  
DTALRLAAYL GPDPQFWLNL QTHYDLSVTY LDARTLLEAI KPYDRQQNVA RTLNPLQESS  
Q

> RXA00990 (1-453, translated) 151 residues  
VATDIAARGI DVDDVSLVVH VDPPAEHKAY LHRAGRTARA GTSGTVVTLV MDEQIKEVRE  
LFQKAGVTAA EVKVNENSPE LAKITGARRP SGVALPAPGQ QQPKREQKNT HNRSDSRGSS  
RNPRRRQSG SRSTGRSNPR RQTSRKDGPK S

> RXA00994 (1-342, translated) 114 residues  
MTTFLELKLP DEIVRELRSQ GITEAFPIQE AAIPDALAGK DVLGRGPTGS GKTFTFGLPM  
ITRLARSGAS KPGRPRGLVL VPTRELAAQV RERLDDPARV MGLRVLEVVG GVNI

> RXA01030 (1-1176, translated) 392 residues  
MTSTTQPGTT PELSADTHSE PWDVVIEN TL EPFQKVVRQF IIDRPYSGIF LTMGGGKTLT  
TSLALTYIQP PGHILVVAPL NISRLTWPEE VRKWNIPVNA ISLITNERGT KLTRAKRLKL  
YEETATTPPT LYYITINLLE DIVNYFGDRW PFWTVIIDES QTISDISSKR TRALFSVRPY  
IGRLILLTGT PSANKFDSIY AQVAVLDYGA SLGDNIDVFR ARWCAPDIIT DKQVRRWKPA  
NKQAEAEVYR TISHLVMSAV NTDIKLPPLH FVDHEVHMSD DEHRDYELFK KDAVLAALLD  
MAEENEGGEG ADDTDAADSA TTPPASSQP TNPAIPAGLL QAIQQTQDTN GRAIAPVTTA  
ELDHFDLDPV QRQEDLGT LV VISAVHASDS AA

> RXA01064 (1-636, translated) 212 residues  
MSLSISFHKI ALSATLLGA VAISACALVT QAPPINAAPV TGSSSLSFTL DLGTTTPTSI  
DTVKLTQQAQ NQAAPRVAAS LVRVVDGDTI VVNYQGAQKT VRMIGIDSPE TKHPTKPVGF  
YGPSSQNLT TMLRGATITL EFDSTQARED QYGRLLAYVW YTKGDSGLKL ANLEQIASGS  
AAEYSFDTRY NHRNIFLRAQ TLAKASSLGM WG

> RXA01149 (1-258, translated) 86 residues  
VVAPQSRKPQ HPGEILSERF LEPRGISHYD LAKTLHITEA TIANFVEGRT DLTIGLAVRL  
SRSFDLSTQE WIALQRTFDQ AHRRSA

> RXA01157 (1-1605, translated) 535 residues  
MSFSAEKGTH LSEFIADLGF DLDEFQIKGC HAVEEDHGVL VCAPTGAGKT IVGEFAVSLA  
LSRGTKCFYT TPIKALSNOQ YHDLVAKHGS DAVGLLTGDV SINHDADIVV MTTEVLRNMI



YAGSFALERL SHVVMDEIHF LADASRGAVW EEVILNLDD S VNIIGLSATV SNSEEFGEWL  
 TTVRGDTRVI VTDHRPVPLD QYMMVQRKVM PLFEPGTDGR VNKELEATID RLNSKQSEQG  
 RAAYRSGEGF RARSKGDKQD SRTGKPREQD RHRPLGRPEV LSILKGINML PAITFIFSRA  
 GCDGALYQCL RSKLVLTQDA ESEEIARIVD AGVVGIPEED LQVLNFKQWR AALMRGFAAH  
 HAGMLPAFRH IVEELFVKGL VRAVFATETL ALGINMPART VVLEKMKVFD GEGHVDLTPG  
 QYTQLTGRAG RRGIDVLGNA VVQWSPALDP RWVAGLASTR TYPLISTFQP GYNMSVNLK  
 TIGYEPSLRL LEKSFAQFQA DGSVVGDVRE IERAEAKVAE LRAQLNKEIA ATNPA

> RXA01238 (1-1401, translated) 467 residues  
 VIAAYGASIS LDDSTLTISY SPLLAALSKS SAQSESVDLT QVSGVSVQDP TAFTHGFLNL  
 EGVDKSIAFA PNSSADLAAL AADIDAVLKG EKPQHLGGGA PVVPSAPSTV AGLNFVGFVDV  
 ETANDDWGSI CQIGLVKYVD GVEESSESWL CTPPESLNFF NEINIGIHGI TPEMVADQPR  
 FADLVPKMVE FVGDLPLVAH NAQFDFLTALS RACAASGIDV PEMIYGCSLT LARNEKLQVE  
 NHKLPTVASH LGFELKNHHD AAEDARACAA ITIALAKRHS FECSFVDFVH SRGFTMGTV  
 NARVYPVLKD RSGANVALQR RNFGLDAGKT EVPVQPAVDP AWETPKAEPK KQSGRRAPWD  
 KVATPEVIPD PNPDA DPSSI LYGQNVTLTG DFEPYEKGAL WQRIADQ GAL IGKNVTKKT  
 ILVAGPWATI TSKQKRAEEL KEKGQDIQIW DEKQLFTALG LDEQPPF

> RXA01255 (1-1080, translated) 360 residues  
 MSTTSESQDH AARIEAERQE AIEAAPFVSV SIQSSGIHPS TSRMVTIDL V TLSPNLEPVE  
 TFHAVLDSKT DPGPFHLHGV TEEEFASAKR FGQILKSLDR LIDGRLLIH NAARSWGFI V  
 SEAKRAMNDA ARANRNSNRG NRRGGRGRRR QRVGHIPKPL VIVDTLASAR RQAIALDDVR  
 IRGVAHTLGL DAPAAEASVE RAQVSHRQLC REETLLVARL YGALKQSGPL AEIDPQSLRA  
 DKFGLQRSII RVQAQEASPT LVNPGTYEPG KTLIAGMEVV VAPEIEMDPD IIIQACVDAD  
 LSYSEKLTRQ TSVVVCNQTR DIDGKAMHAQ RKGIPLLSDV AFLAAVKRVK EGKKVDVEKR

> RXA01279 (1-465, translated) 155 residues  
 MRKSAAPKRP VVQDPVYKSE LVTQLVNKIL IGGKKSTAER IVYGALEICR EKTGTDPVGT  
 LEKALGNVRP DLEVRSRRVG GATYQVPVDV RPERANTLAL RWLVTFTQR RENTMIERLA  
 NELLDAANGL GASVKRREDT HKMAEANRAF AHYRW

> RXA01280 (1-366, translated) 122 residues  
 MPTIQQLVRK ARHDKSDKVA TAALKGSPQR RGVCRTVYTT TPKKPNSALR KVARVRLTSG  
 IEVSAYIPGE GHNLQEHSMV LVRGGRVKDL PGVRYKIVRG ALDTQGVKDR KQARSRYGAK  
 RG

> RXA01286 (1-654, translated) 218 residues  
 MENEIKGIL GTKLGMTQIF DEENRVIPVT VVEAGPCVVS QIRTVETDGY NAIQIAYGEI  
 DPRKVNQPLT GHFKKAGVTP RRHVTEIRMD DVSGYEVGQD VTVEIFNDIK FVDVTGTTKG  
 KGYAGAMKRH GFAGQGAGHG NQAAHRRVGG IGAAATPGRI FKGKRMAGRM GNDRVTTQNL  
 KVQKIDADAN IILIKGAIPG NRGGIVTVKT AVKGGAHA

> RXA01287 (1-303, translated) 101 residues  
 VAGQKIRIRL KAYDHEAIDA SARKIVETVT RTGARVVGPV PLPTEKNVYA VIRSPHKYKD  
 SREHFEMRTH KRLIDILDPT PKTVDALMRI DLPASVDVNI Q

> RXA01305 (1-1866, translated) 622 residues  
 MRPSSRPLGL VLCTALASTI ITVPAASAQE PALLDASAIA PHTASYGYV DAWDTNVSTD  
 LNPSSNAAVG VLEEMLELWT PGEEWNTGVK VDPTVLDSNI AQSV AISQQA TDAQQERAWV  
 IDRRNQNYTA TDGLGAYADS YRETAQVGT IPDVVPADAT TVKYNDGGNV NGNWAETGGE  
 LGSTVDLIEA IRQHAATSNN AKAYYQYPRP YRWTESIEPE AWGEGVDMPE YANPLRKDES  
 EAASDGGFPS GHTSAGGMAT NGLAYAFPQQ YDKLLMTAAE IGESRIQLGM HSPLDVIGGR  
 VLSTAITAGA LNDPNLDSVK AEAFFDQAQW ISNQSDITTN TRDFDEQLAE YTNFLTGFGE  
 QSGDTTQDMR VPKGA EALLE TRLPYLDDEQ RRWVLHSTGL ESGFPVLDDA EGWGRNLNLYA  
 AQAGYSAFDT NVDVTMNAID GGYNAKDNWQ NDIEGAGSLT KNGSGELTSL GDNSYTGTT  
 ITAGTLVAAT ESALGAGDLT INDGATLKIT QPVTVDGTAN LGGTLHVALP VGTNHVTVID  
 AASISGEFDE VIVDGA VDAQ VSYDNGSVVI TTGAPSDDVK ETGSSAGGIL AIVAALGGIA  
 ALIFGAFTQF GFPPAIKEMF DL

> RXA01334 (1-384, translated) 128 residues  
 MAKLTKEDEI EAFKEMTLIE LSEFVKEFEE VFDVTAAAPV AVAAAGAAGG EAAAAEEKDE

FDDVLEDAGA KKIGVIKAVR ELVSGGLKE AKELVEGAPK AILEGANKDD AEAAKAKLEE  
AGAKVTLK

> RXA01335 (1-513, translated) 171 residues  
MANPRNEAAL AELKARFAET DTVVLTEYRG LTVAQTTELK KALGFDVQYS VAKNTLVKIA  
ANEAGVEGLD DLLTGPTAVA FIKGEAVDTA KVLKKFGEEN KAFVVKGGYM DGNALTAEQV  
NAIAELDNRE TTLAKLAGAM KGSLAKAAGL FNAPASQVAR LAVALQDKKD A

> RXA01343 (1-651, translated) 217 residues  
IYSPLEAANL VKETSSKNYD ASIDVAIRLG VDPRKADQLV RGTVSLPNGT GKTVRVAVFA  
QGEKATEAEA AGADFGVTDE LVEKIQGGWT DFDVAIATPD QMAKIGRIAR VLGPRGLMPN  
PKTGTVTNDV AKAIEEVKGG KISFRVDKAS NLHAAIGKAS FDAKKLAENY GALLDEIIRI  
KPSSAKGIYV KRVTLSSSTG PGVEVDTHVT KNYAEEA

> RXA01353 (1-339, translated) 113 residues  
MNILDKIDAA SLRDDVPAFR AGDTLDVHVK VIEGTTTTRTQ LFKGVVIRRO GGGIRETFTV  
RKVSFGIGVE RTFPVHSPNI EKIEVIRRGD VRRAKLYYLR ELRGKAARIK EKR

> RXA01356 (1-627, translated) 209 residues  
LSRNLGPVA GVDEAGRGAC CGPISIAACI LPDKPIQELA ALTDSKKLSA STREKLMPLI  
KKHALAWSVI VISAQDIDRF GIQHANISGM RRAVAALGTQ PGYVLTDAMK VPGFTVPYLP  
IIGGDASARC IAAASVLAKQ TRDDIMTDMA NDYPHYGLEI HKGYSTKIHM DAVRHHGASP  
EHRYSYANVA KAHQEWLHAA DNDTTEGGA

> RXA01363 (1-699, translated) 233 residues  
MSSLIPVHAA GSIQEGITEY LTTSFSLADK QVATELKRFL GHGDSGMFHG PYVRARLPYA  
QAQEWENVLS WLPENFVPYH HQKAAFQRLS SLDNRGKDRR PDPTLVVTGT GSGKTESFLY  
PILDHALRLR KRGQQGIKAL LLYPMNALAN DQADRLARLI HNNPALKGVT AGIYTGEAKG  
NRTQMGEREL INDPQAMRVS PPDILLTNYK MLDQLLLSV DREMWOXSAT SLQ

> RXA01374 (1-882, translated) 294 residues  
MSESGALSST DSLSPGVTE VRDEIWLVT VTRSTDGFRV KARGLSDYVR DHEATFFTAL  
DKDLKVIDPT QVTVSLDDSS NYRRTLRLWE ATMRKTPVPL YQESLSVADQ MLADPLEYQL  
AAVRKTLSSA NLRPRVLIAD AVGLGKTLEM GMILAEIIRR GRGERILVVT PRHIMEQFQQ  
EMWTRFAIPL VRLDSVGIQQ VRQKLPASRN PFTYFPRVIV SMDTLKSPKY RAQLEKVHWD  
AVVIDEIHNA TNAGTQNNEL ARTLAPTAE LILASATPHN GDPESFKEIL RLLD

> RXA01423 (1-141, translated) 47 residues  
MAKGKRTFQP NNRRRARVHG FRLRMTRAG RAIVAARRRK GRAKLTA

> RXA01424 (1-309, translated) 103 residues  
VHLWDSAESL DGTEKQGEVA SFGGPRFGLV VSKAVGNAVV RHRTSRRLRH ICASIAEKSP  
ELLSPTHHV IRALAGAGNA TSAELERDIR YGLGKASVR TNK

> RXA01453 (1-297, translated) 99 residues  
MAQKLYPPIH PGEILMEDFI KGFGLTQNKV AVSIGVPPRR INEIVHGKRS ITADTALRLG  
RYFGIDPQFW LSLQTQYELE LDRDAGAATY AQITPLKVA

> RXA01480 (1-1893, translated) 631 residues  
MAKGRIPESD IQAIRERTPI EEIVGDYVQL KSAGADSLKG LSPFKDEKTP SFHVRPNRGY  
YHCFSTGKGG DVFSFLMEME HISFPEAVEV CAEKIGYQIN YQGGGPGRRE EPGTRQRLIL  
ANKAAHQFYR EQLETPEAQP GRELLQRGF GQQHIYHFEC GYAPAGWDTL TKHLLKKGFE  
FKELEAAGLS KMGKRGPIDQ FQRRLLWPIK NLSGDVIGFG ARKLFDDDKM GKYMNTPETL  
LYKSKSVLFG LDSAKKAAIA GHQAVVVEGY TDVMAMHAAG IDTAVASCGT AFGEHLQML  
RRLMLDDNYF RGELIYTFDG DEAGQKAAMR AFEGDQKFTG QSFVSVAPNG MPDCDLRLER  
GDAAVRDLVA RRIPMFEFVI QSIISEYTLT TVEGRLAALR RAVPIVADIR DKTLOSEYAR  
LLSGWVGWSD PSEVLQVHE EARRPKRDKK PVRAKRFDQP LEDQSLRPTM ALPNPRNPVL  
WQERESLKIA LQYPELAGSY FDGLPTDSFT NPAYRMVRDA ISAAGGCERA LDGTDWLPV  
SENMTDILGT SLVSELAMEP IEVEAQDLES YTDGVLRLQ ETRVGNQIAI LKQQLQMRP  
SEDEQAYNSL FSDLVALEQA RRELLARAFA G

> RXA01481 (1-492, translated) 164 residues  
MQNSKKTLLG VLGIVVLA AWFGIDLSTS GEATSQASSS ATTTITSSN TPTSESISSN  
SDLDGDSM SELPQEADEV VDDILAGGPF DYPDNDGVRF GNYEGVLPKE SSNNYYREYTV  
ETPGLSHRGP LRIVTGGSNP TDPEVWYYS DHYETFCAT DAEN

> RXA01487 (1-267, translated) 89 residues  
MALTSEQKKS ILSEFGLHET DTGSPEAQIA LLTNRRNNLT EHLKFHKHHD HSRRLGLLLV  
GRRRLGLLKY ADNNVDYRD LIARLGLRR

> RXA01495 (1-447, translated) 149 residues  
MADNARAARM AKRIQTIVAS AIERDIKDRR LEFVTITDVT MTGDLHDAKV FYTVRGASIE  
EEPDLAAAE ALHRARGQLR KIVGQQLGVR FTPTLTYSID TVPEASAHME ALLDRARKRD  
EELAKLREGA APAGDADPYK TSSKSESEE

> RXA01563 (1-810, translated) 270 residues  
QIFDLHLLKG HGSEDWSKRP LPESWLNAAA LDVEMLLLELA DVMAEILDQQ GKLPWAEQEF  
VHIVDQFATM TEPSETSWQD LKGLSTLKR DQLVVAREMW LERDSFAASR DLAPGKVLN  
KVIVEVARVL PRTPAELAQV KGFPGRSQGA TKRWFRITR ALKSPRRNWP KPQQRKDGIP  
DRRAWASYYP EEHEVLQEIR ALIDDLAADI NVPGENILQP STLRVAVWMA KHTGEIHNAE  
TLNAVLRDYG ARQWQIDQTF PILSANLLKL

> RXA01568 (1-435, translated) 145 residues  
WDNITYLMRA ARKGTVVPMV IELDGRFVGQ LTIGNIQHGG ISDAWIGYV SSALTGRGIA  
TAACALGVHD AFRRLGLHRL TATYLPNPA SGKVLGHSGF RPEGLIRNL HIDGQWMDH  
FVALLADEYS ITAVERLTRE GLRR

> RXA01581 (1-813, translated) 271 residues  
MALDFNEAFT ERTPRIVNAA KLHRAAQRKK DKRFLVEGEN SVEAAVATGA ATDLFVTESA  
AERFEEIVRT AGYMNVTYTHA ITDKAAKHL DTVTITGIFA LCDDVLWSVG KAITGQPRLV  
SVPVETREPG NAGTLIRVSD AVGADAVVFA GESVDPLGAK AVRSSAGSLF HIPVARNNNI  
ADVGLQLRSK GLQILATSAD GEVDLDDADE LLAKPTAWLF GNEAHGLDES LLAQADHRVR  
IPIRGRAESL NLATAASICL YESSKALFAG E

> RXA01594 (1-744, translated) 248 residues  
MIRGRRVFVA GMLALKPATV VEPEVSIRVE EDASEDWASR GAHKLLEGALE SFEPLGLKVK  
GRRVLDAGAS TGGFTDVLLR REASEVAVD VGYGQLIWR QNDDRVRVVD RTNIRYMTLE  
DTGGCEDMMV GDLSFISLKL TLPAIAKVLS DGADLLPMVK PQFEVKGKDL GSGGVVRSPE  
LRAEVTADVA KFAATLGLSL KHVVASPLPG PSGNVEYFLW LVKDGGASMP DDQQLSAMID  
TAVKEGPQ

> RXA01637 (1-309, translated) 103 residues  
VREASVEKQP ASSDPLETIR SRWSELNIV EKQSVRTSIM LTEARVLGLR GDTLVLGHST  
GALAARLNAA DHNGILVKVL AEETGLQLKV ECIVGTNP AE AGF

> RXA01661 (1-666, translated) 222 residues  
LDSTNTPGPT EWGESRVGKG PWEEENPGVP RPTSPLFDVT LLNEGDRRN VDAYRYWTRE  
AIVEDIDTRR HSLHVAIENF ENDANIGTV RTANAFVNT VHIVGRRRN RRGAMVTDYR  
QHLMHEDVD SLLAWAIAER LTIVAIDNTP GSVPLETAE PKNCLLLFGQ EPGVTEAAR  
AGALMTCSIA QFGSTRSINA GVAAGIAMHA WIRQHADLSQ AW

> RXA01682 (1-234, translated) 78 residues  
RTKVDAYKSQ KRGGKGVCGA ELKQDDIVRH FVSSSTHDWI LFLHQLRSRV PPQGIRTSRG  
IPHRTWTARG QPSGIPTW

> RXA01683 (1-750, translated) 250 residues  
VYRLKAFELP EASRTARGQH VANLLEFQPG EQIAQVIQLE SYNDFFPYLVL ATAHGRVKKS  
RLLDYESARS GGLIAINLNE DDRLIGAALC GEEDDLLLV EFGQSIRFTA DDEQLRPMGR  
ATAGVKGMR RDNDQLLSMS VVRDGEFLV ATSGGYGKRT PLEDYSTQGR GGLGVVTFKY  
TPKRGRLVSA IAVEEDDEIF AITSAGGVVR TEVKQIRPSS RATMGVRLVN LEEGVELLAI  
DKNVEDQGEA

> RXA01684 (1-873, translated) 291 residues  
 GDTAIYDTLV RMAQPWSMRY PLVDGQGNFG SRGNDGPAAM RYTECRMTPLE AMEMVRDIRE  
 NTVNFSPNYD GKTLEPDVLP SRVFNLLMNG SGGIAGVMAT NIPPHNLNEL ADAIFWLEN  
 PDAAESEALE ACMKFVKGPD FPTAGLIIGD KGIHDAYTTG RGSIRMRGVT SIEEEGNRTV  
 IVITELPYQV NPDNLISNIA EQVRDGLKVG ISKIEDESSD RVGMRIVVTL KRDAVARVVL  
 NNLFKHSQQLQ ANFGANMLSI VDGVPRTLRL DQMLRYYVAH QIEVIVRRTQ Y

> RXA01688 (1-564, translated) 188 residues  
 QFEGQTKTKL GNTEIKSFVQ RMANEHIGHW LEANPAEAKV IINKAVGSAQ ARLAARKARD  
 LVRRKSATDL GGLPGKLADC RSKDPEKSEL YIVEGDSAGG SAKSGRDSMF QAILPLRGKI  
 LNVEKARLDK VLKNAEVQAI ITALGTGIHD EFDINKLRYH KIVLMADADV DGQHIATLLL  
 TLLFRFMP

> RXA01689 (1-726, translated) 242 residues  
 FSDSYAVSG GLHGVGISVV NALSTRVEAD IKLHGKHWYQ NFEKSVPDEL IEGGNARGTG  
 TTIRFWPDAE IFETTEFDDE TISRRLQEMA FLNKGTLTITL TDNRATDEEL ELEALAEQGE  
 TATELSLDEI DNETELVEET TDAPKKPKKR EKKKIFHYPN GLEDYVHYLN RSKTNIHPSI  
 VSFEAKGDDH EVEVAMQWNS SYKESVHTFA NTINTREGGT HEEGFRSALT SLMNRYAREH  
 KL

> RXA01713 (1-354, translated) 118 residues  
 MVSDLLQPRD GIPPLLSTPG EFTAAADLLA SGTGPFADIT ERASGFRYDD RAFLIQIRRR  
 GSGTLLFDPE QFRPELTQAL KPVINGQEWI IHAASDPLPS LAWLDLHPGL LFDTELAG

> RXA01718 (1-486, translated) 162 residues  
 LLTAVLSLIA GLVVIGVIV LNGYFVAQEF AYMSVDRNEL RALADSGDKK ARRALSITKR  
 TSFMLSQAQL GITVTGLLVG FVAEPLVGNA LGVLLGGVGV PAAVSISVGT VLALAISTVV  
 QMIFGELFPK NYTLATPLKS ALALAPSTTW YLKPRWLVDH IL

> RXA01735 (1-282, translated) 94 residues  
 VANTEHNYDA SSITILEGLE AVRKRPGMYI GSTGPRGLHH LIWEVVDNSV DEAMAGHATK  
 VEVTLLEDGG VQVVDGGRGI PVDMHPSGAP TVQV

> RXA01736 (1-2868, translated) 956 residues  
 TVSTYDSYAG TLIREYGLLL PVEPSARLIT QTELYHIARN VVNNYDGELT ATQTPATVTE  
 YLLKLVSEMD NHMVTAEDIR EESDPFIKLF DELPKGKGQR DNLNAEMTKW RDTQVARLQY  
 LPLVKALKEE LHNQAVVTFG EQMSKAAHLA STHPQVGYSQ RRRFRVVMLD EYQDTSQSQR  
 VLLSSLFGGT DPGLTVNAV G DPMQAIYGWR GATAANLENF VDDFPVIHLD GKTRAPKNEL  
 TTSWRNPPEV LTLANAVSRE VLGSPDAPTR TVQPLQPREG APTGEVSLGW FGTAQEREF  
 VADEMVKHVN AREEKGTFTA AVLVRKKRHS APMAEELTKR GIPVEIVGLS GLLDIPEIAD  
 LISLATMLVR PHDNRAALRI LAGPHVGLGV ADLQRLQGRA RNIAGRVSRE RREKNPDPLA  
 ELDAIIEEAT AIEPEAVVGL ADAVADLGE G DRFSEEGLSR LKRLATQLRY LRKYSLGRSV  
 ADIFADIETV FNIRTEVLSR QDPHADGAAG TVHLDKFAGE VASHGGIGLP ELLDYFELAK  
 DQEEGLEPGE VTVRSRDRVQI LTVHKAKGLE WDIVSVLHAD ASTYDAKAST WLKNVTMIPS  
 SLRGDAGTGA PEMDTSEADD RKALED SGKE YTSEVREGLR EENSRLFYVG ITRSERVLLV  
 TGSALDESGT KAKVPYGHLE ILRDKAPECV VSWWEGEEGD VEKQKPAEGV FPQLLAADSS  
 GADLVRGPRA EPNNEGGLES LWEKEVSALI DEHRRLSNPI VEVEPRELT ATDLVSMKNN  
 PEQFARRMRR PVPFKPNTYA KRGTLFHQWL EDRFGSTALL DETELPGIDE DYSDDAFIEL  
 RDAFLGSTWE NRTPEFVEHP FEVTIGEHVI RGRMDAVFHT DGTWMVVDWK TGRPTGPPEM  
 DAAIIQLAVY RLAWARLKGL EPEEVRAAFH YVAHDHTFEP NDLPTQEELA RLLSQE

> RXA01739 (1-597, translated) 199 residues  
 VINLQDLDED QRIAASAPRG PVCILAGAGT GKTRTITYRI AHLIDQGFVS PNRVLAVTFT  
 SRAAGEMRHR LNLMGIGGVQ ARTFHAAARK QLLYFWPQVA GNLPWRLLDN KFQLVGRAVR  
 GARLESQTEK VRDILGEIEW AKASLITPEQ YPDRLGTRTP PAPAEEKIAEV YQRYENMKAT  
 PEGMLLDFDD LLLHTAGAL

> RXA01740 (1-1422, translated) 474 residues  
 VAEFEFRQQYR SFVVDEYQDV TPLQQRVLDA WLGD RDDLTV VGDANQTIYS FTGATPEFLL  
 NFSRKYPEAT VVKLQRDYRS TPQVTALANT VIGQARGRVA GTRLELQGM R IAGPEPEFSA  
 FDDEPTEARE VAGRILTLLK NGVQASEIAV LYRINAQSAV FEQALADAGI VYQVRGGEGF

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FTRPEIRQAL SQLIRTSQRD VDESDLVRLT QRTLVPPLGLS SEEPSGAQER ERWQSLNALV
DLVKDLVKAT PDLDLTGLLL KLRERQEAKH PPTVEGVTLA SLHAAKGLEW DAVFLVGLVD
STLPISHAIK SGDEAIEEER RLFYVGVTRA REHLHCSWAL ARQEGGRKSR KRSRFLDGIV
VEMASESGTP RSNRPKNCRV CGSVLSSPAE KAVGRCASCP IQADERVFEQ LRTWRNDTAK
RENKAAYMVF SNATLMAIAE MNPTNENELL SVPGVGPMKI ENYGDDVLAI LGAL

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> RXA01772 (1-2364, translated) 788 residues
FKKAFKKQSE ALGIVYTPVE IVDFILRAAD DVSKKHFGRG LSDKDVHVLD PFTGTGTGMV
RLLQSGLIK PDLARKYANE LHATEIMLLA YYVAAVNIET TYFGLEGERA LRNGEDAPVY
EPFDGIVLGD TFQMYEDDDK LDLDVFTANN DRMERQRLTP VQVIVGNPPY SVGQSSANDN
NANLKYPTLD RRIEDSYAKY STATNKNSLY DSYLRAFRWA TDRIHTQGVV AFVSNNGWVD
GNTADGVRLS LAQDFSEIYV FNLRGNSRTG GD LAKREGGN VFNVRVGTQI IVAVKNPQLS
GCRILYKDIG DNLSADAKLN EIAVATIEGA EWQTISPNEY GDWISQRSVD FDTWPVLGDK
KNKSALKVFQ TFSAGLKTGR DAWCYGPTSA QVKTNITRLL ETYEQAQRF NSWVVDNGVT
SPKEADVNFQ LKQNPDLADS KKISWDSNLK MSLSRGDTFS FDPSSIQMSL YRPFPPQQT
FHVSLNQRRY QLPSMFPTPE HDNQGFYIVN PGSAPFSTL ATNLLPDLAM WGSNAGQFFT
RWTWEPIETR EGELDFGNGL FSTTPKKGVE GEILDGYRRV DNITDEILKL YQSSLGEDVT
KDDIFYFVYA QLHDPAYREA YAADLKKMLP HIETPTDRAR FDHFVTAGKE LMDLHINYED
VEPWDVEVKV KEKADPTDRE TWRVTMKMKA KVRDPETKKL VEDHTTLIYN SSITISGIPE
EAENYQLGSR SAIWLIDRY QVKKDKASGI VNDPNDWADE VGNPRYIVEL IAKVTRVAVE
TMRIVEEL

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> RXA01786 (1-441, translated) 147 residues
MRAAKITRGF TSNPAGSVLV EFGNTRVMCT ASVELGVPRF KRDSGEGWLT AEYAMLPAAT
AERNRRESMA GKVKGRTHEI SRLIGRSLRA AVDLSQLGEN TIAIDCDVLQ ADGGTRTASI
TGAYVALADA IKVLQERGVV PGSPLLA

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> RXA01797 (1-708, translated) 236 residues
GSIAWIDLTP EDRSAYDDQV RQGSWMGMRR SAMLSPTPRL TSAKMQRILE LFEEAEEHGR
KALIFTYFLD VLDELEKHLG ERVIGRISGD VPATKRQLLV DALSHSKPGS ALIAQITAGG
VGLNIQSASL CIICEPQVKP TIEQQAVARV HRMGQTATVQ VHRLLIGETA DERMLEILAG
KTHVFDVYAR LSETAEIPDA VDITESQLAA RVIDEERARL GLTESTGPKD EETALS

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> RXA01824 (1-822, translated) 274 residues
MKETDNLLRE NSHDRDISEI VATITALDHP SPSLLRFTAF VPGSANNPVW AEANVAIRLY
LSEEFDDATR VYTVRSFDAA TESIVVDVVQ HHESPMMRW SDTVKINDTL VLTGPRPHFV
IPEGEQAALF LDDTAIPALA AILDQWPTDL RGKGWVVTDD PAAFDELPSI DGLELNLAP
GSDPTVQPLA QQAYDLENPE TYVVWAAGER DEIKSIRRHF RKQVGLEKDA VAVFGYWKYN
TTNTQIDAVR KENYMKMLSE GLQLENFDDL SLEI

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> RXA01832 (1-894, translated) 298 residues
MATSNRIANA MNSLAKLDSS MQRGLDNALA FVFRGRVPA ELEELLKQEA EDNVVHTEFG
YVEAPNVFKV SVSPNDFSNI VDRFPDQPAR FGDQMMRFCR NSGWTLVGPV IVLIEEDSSL
HTGQLKSVSE KDPDPSELSS YLPLEGDGIL PVAESESKNV SDSSPYTGTE FLPAQSAADRP
LVQGVPSQV DANRQAAMKP AGPTVTLLLQ DGSSRTYLVR EGSNIIGRSN DADLRLPDTG
VSRQHVEITW DGRDAILVDL KSTNGTTVND TPVDNWLAD GDVITVGHNS IEVRIVSP

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> RXA01866 (1-321, translated) 107 residues
LKPGRHDDGV TVLIPIVPLG GLDTEGFDWL VPGLRLDLVT ELIRTMPKAL RRTVVPAPDF
AERVLPLLRP YMTPLTTQLA DALHTLGGQG INASDFDPAK LPDHLRI

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> RXA01867 (1-492, translated) 164 residues
PEWVEKAAGP LLKHQYSEPY WSSKRGAMV HRKSTLFGVT IVAVKVVPYH TVDPVAARDM
FIRHALIEGD WSTHHRFYHD NVAKLEAIGE LEAKARRRDI VVDEDTLFDY YDAKLPSNAT
TTRNFDSWWK KTSRVTPDLL DFDPSLIKE DAGALRRSL RQVD

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> RXA01876 (1-1473, translated) 491 residues
IIGPNKTFLE YISHVLPELG ETGVVLSTVG ELFPGIVPTG SEDTLTREIK GSEEMASILA
EAVKAYQVLP EKTIVVSVDG IEISIDEKTV AKSRRARRA RQSHNSARPI FREHLVEQLA
HQMAQTIGAD PLGGKNLLSA ADIDQLHDDL LDDAALQSVI DDFWPELRPQ DVLHDLLEISE
ERINVAAGY DEETKSALLR GELDPWAPSD AALLDELALL IGLPDPEEAR EKAEAKWREQ

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IDDAQEVLVDV LSSSQSSDID DVTEAEVLSA FDVIDAETLA QRQTVTDNRT TAERAQADHK  
 WAYGHVIVDE AQELSPMEWR MVFRRSPSRW MTLVGDIQQT GWPAGVDDWA ESLWPFVEKR  
 FRHHELTVNY RTPAEIMSV A NELLTQINPD IAPAMAIRES GREVVNLPLD ADLSAVMDSL  
 REEDSQRTIA VISSRRHHES DFYLVD DIK LEFDHVIVVD PAGIVEESPQ GLQDLYVAVT  
 RATQSLTILG E

> RXA01893 (1-555, translated) 185 residues  
 MIDEILFEAE ERMTATVEHT REDLTTIRTG RANPAMFNGV MAEYYGVPTP ITQMSGITVP  
 EPRMLLIKPY EMSSMQVIEN AIRNSDLGVN PTNDGQVLRV TIPQLTEERR KDMVKLAKGK  
 GEDGKIAIRN IRRKGM DQ LK KLQKDG DAGE DEVQAAEKEL DKVTAGFVAQ VDEVVARKEK  
 ELMEV

> RXA01912 (1-771, translated) 257 residues  
 MRRFIFTERN GIYIIDLQQT LTYIDQAFEF VKETVAHGGT VLFVGTKKQA QEAVQVEADR  
 VGMPYVNHWR LGGMLTNFQT VSKRLNRMKE LQAMDAENG YEGRTKREVL MLTRERTKLE  
 RVLGGIAEMT RVPSALWIID TNKEHIAVAE AHKLNI PVVA ILDTNCDPDV VDFPVP GND  
 AIRSTALLSR VISTAVEEGK KAREERQLAA AKDAAGDAKP EAEAPAAAE AEEAPAAEAE  
 EHLQLSKLPL TAVSAVS

> RXA01948 (1-603, translated) 201 residues  
 SVELPAEIFD REVSVALLHQ VVNAQLAAAR QGTHSTKTRG EVRGGGRKPF RQKGTGRARQ  
 GSIRAPHFTG GGISHGPKPR DYSQRTPKKM IKAALYGALS DRARNARIHV VSELVPGQTP  
 STKSAKAFIE RLTERKSVLL VVSREDINAQ KSANNLPGVH ILAADQLNTY DVLKSDDVVF  
 SVEALHTFIN RASGAAQEEQ N

> RXA01949 (1-303, translated) 101 residues  
 MATIANPRDI IIAPVVSEKS YGLMEQNVYT FFVSTDANKT QIKIAIEEIF GVKVASVNTV  
 NRAGKRKRSR TGFGRKATK RAYVTLREGS DSIDIFSGSV A

> RXA01950 (1-384, translated) 128 residues  
 MAIRKYKPTT PGRRASSVSM FTEITRSTPE KSLLRPLSKT GGRNSHGHT TRHRGGGHRK  
 RYRVIDFRRN DKDGV LAKVA HIEYDPNRTA NIALASLLRW REALHP RTEG PDPGHRYRVR  
 RCSRHQGW

> RXA02037 (1-330, translated) 110 residues  
 GKKGPLYAPN VDCGDHVIVI NADKVAVTSN KREREMRYRH SGYPGGLKSM TLGRSLDLHP  
 ERTIEDSIVG MMPHNKLTA SAKKLHVFSG SEHPYAAQKP EAYEIKKVAQ

> RXA02038 (1-309, translated) 103 residues  
 MSEPIQNENV ESNVADAADI AAATAATEEF TNTIGDAIAT ASEETIEAA PVVLDGPIQT  
 VGRRKRAIVR VRLVAGSGEF KCNGRTLECY FPNKLHQQLI KAP

> RXA02041 (1-714, translated) 238 residues  
 RLGITSDWKS HWYADKSYAD YVAEDIKIRE FLSKGLDRAG IADVVIERTR DRVRVDIHTA  
 RPGIVIGRRG AEADRI RREL EKLTKGQVAL NILEVKNVDA NAKLV AQ SIA EQLTNRVAFR  
 RAMRKAIQSA MRQPQVKGIK VVCSGRLGGA EMSRTERYHE GRVPLHTLRA EIDYGT YEAH  
 TTFGRIGVKV WIYKGDVVG RRESEINAPA ERRGRGDRNA RPRRGQRRQ RAEQKQEG

> RXA02042 (1-414, translated) 138 residues  
 MLIPKRVKYR RQHRPTRSGI SKGGNRVTFG EYGIQALEPA YITNRQIESA RIAINRHVRR  
 GGKVVINIFP DRPLTQKPLG VRMGSGKGPV EKWVANIKPG RILFEMSYPD EATALEALRR  
 AGQKLPCVKR IVKREDQL

> RXA02043 (1-141, translated) 47 residues  
 MAIGTPAHEF RELNEEELVT RLNEAKEELF NLRFQLATGQ LTNNRRL

> RXA02077 (1-396, translated) 132 residues  
 MLGKGELLTE GRSKDSILAD TTEALFGAIF RQHGFETARD VILRLFAYKI DNASARGIHQ  
 DWKTTLQEEL AQRKRPMAY SATSVGP DHD LVFTAIVTLE GEEMGRGEGP NKKLAEQEAA  
 HQAFRKLRES RA

> RXA02145 (1-1617, translated) 539 residues  
 MSLATVGNL DSRVTMASGI RRQINKVFPT HWSFMLGEIA LYSFIVLLLT GVYLTLLFFDP  
 SITKVIYDGG YLPLNGVEMS RAYATALDIS FEVRGGLFIR QMHHWAALLF VVSMVLHMLR  
 IFFTGAFFRP REANWIIGVV LIILGMAEGF MGYSLPDDL SGVGLRIMS IIVGLPIIGT  
 WMHWLIFGGD FPSDLMLDRF YIAHVLIIPA ILLGLIAAHL ALVWYQKHTQ FPGAGRTENN  
 VIGIRIMPLF AVKAVAFGLI VFGFLALLAG VTTINAIWNL GPYNPSQVSA GSQPDVYMLW  
 TDGAARVMPA WELYLGNYTI PAVFWVAVML GILVVLLVTY PFIERKFTGD DAHNNLLQRP  
 RDVPVRTSLG VMALVFYILL TVSGGNDVYA MQFHVSLNAM TWIGRIGLIV GPAIAYFITY  
 RLCIGLQRSD REVLEHGIET GIIKQMPNGA FIEVHQPLGP VDDHGHPIPL PYAGAAVPKQ  
 MNQLGYAEVE TRGGFFGPD EDIRAKAKEI EHANHIEAN TLRALNEANI ERDKNEGKN

> RXA02179 (1-828, translated) 276 residues  
 MTTRTVISDP ADPRLDDVRD LNHSDSRPDL PGGKGLVVAE GPLVVGRLL E SRYPVRAIVG  
 FKNKLD SFLD SIDASLVEGI PVYEV SRELL AEVAGFDMHR GLLATADRTE EASVAQVLEN  
 ARTVVVLEGV GDHENIGSMF RNAAGMGVDA ILFGNGCADP LYRRVVRVSM GHVLRPLFAH  
 LEGTYTTWQR SLEQLKEAGF HVLSTLPDPE AEHLEDALAG KDKVALLVGA EGPGLTEHAM  
 RATDVRARIP MAPGTDSLNL ATSAIAFY E RDRSQ

> RXA02190 (1-1458, translated) 486 residues  
 MPTNNAPQVA INDIGSAEDF LAAIDATIKY FNDGDIVEGT VVKVDRDEV LLDIGYKTEGV  
 IPSREL SIKH DVDPDEVVEV GDQIDALVLT KEDKEGRLL SKKRAQYERA WGAIEELKEK  
 DEPVTGTVIE VVKGGLIID I GLRGFLPASL VEMRRVRDL PYIGQELEAK I IELDKNRNN  
 VVLSRRAFLE QTQSEVRSEF LHQLQKGQVR KGVVSSIVNF GAFVDLGGVD GLVHVSELSW  
 KHIDHPSEVV TVGDEVTV EV LEVDLDRERV SLSLKATQED PWRVFARHTA VQIVPGKVT  
 KLVPFQAFVR VEEGIEGLVH ISELAQRHVE VPDQVVAVGE EVMVKVIDID LERRRISLSL  
 KQADEDYTEE FDP SKYGMAD SYDEQGN YIF PEGFDAETNE WLEGFDEQRQ AWEARYAESE  
 RRFTAHTAQI ERRRQQAEEA AAEAPAGNYS TDSAEDAPAA EAVEESAGSL ASDEQLAALR  
 EKLGN

> RXA02241 (1-2028, translated) 676 residues  
 VARVLPLLGL PHLDRLFDYR ISEDQHDDVQ PGVRVRVRFG GRLVDAIVMS RTAQTSHGK  
 LMWLD RVISP IVVYPPQTAK LIEQLSDRYG GVRSDLIRSA LPARHAGAE ADTSTSWESL  
 GEVKEPDLSS WSAYQHQS F VDAVLAGTTA RASWQIAPGD DWALALASLA VKVVDG GGA  
 LLVVPDQRDL DRLEAALRGL VAAKQITVLN SGLGPQARYR RFLSVLSGQG RLIIGTRSA  
 FAPVKDLKLA VILNDGDDNL VDP RPYAHA REVLTTRSSL EASSLIAGH ARTAETQLLV  
 ESGWMHNLIA PRDTIRTRMP RIQAVGDSDF QMERDPMARS ARLPGIAFHA VRSALERDQP  
 ALIQVPRKGY VPTLACGNCR TPACRHCNG PVGLPQGSSD LAGVPTCRWC GRPDSRFKQC  
 NCGSPKLRAV VLGTERTAE L GRAFP SVRV ITSGGNKVVD SVENRASIVV STPGAEPFVA  
 NSPERPEKSE KPEHKGAYGA LLLLD TWALM GRQDLRAME ALHKWAAAAT LVHSHLHQGQ  
 VIVVADPSFP AVQSLIRWDM AGAAAQELAS RREVMFPSPV HMAAIDGATA ALESFLDLAE  
 LPDHA EVLGP VDLPPGVSLP GEYDEQRFGP PQRLLRITPL GPRSELGRAL RSAQVARAVR  
 KNDLPLRIQM DPIHIG

> RXA02293 (1-2388, translated) 796 residues  
 MSSRIGNFLI NRISTGLPVE NIIPHLQ EAF SAGPKNLVIQ APPGTGKTTL LPPLVANILC  
 NEGAGNATPT KVLVTAPRRV AVRAAARRLA QLDDSQLGTK VGFSVRGEHI SGSHVQFMTP  
 GVLIRQLLNN PELPGIGAVI IDEVHERQLD SDLLLGMLAE LSQLRDDFSL IAMSATLDSD  
 KFANLLDAQV LSVEAPIFPL DISYAPARAP RLNAKGVDWD FLDHMAQKTH DAVTHSEHSA  
 LIFVPGVREI DRVMSTLKS L GHNNVFPLHG QLSPT EQDRA LAPSQQRII VSTPVAESSL  
 TVPGVRIGVD SGLSRSPKRD SARGMTGLIT SSCAQASAGQ RAGRAGREGP GQIIRCYSEE  
 DFSHFPRFVT PEISSADLTQ AALWLAQWGT SPADLPLLDQ PPHAAWTAAQ QILRLIGALE  
 GDAITSLGHR LSTLPLCPQL SASLLRFGEQ SAKILAVVSE NPQGDVEKQQ PDKREVERLR  
 RLAPASVGKA SAGQIVGA AF PQLIGRKIDN GEYLLASGTR ARLMDSDLKD AEWISVAAIN  
 RSQNSAIIRA AARISED DAI DIIGVVEETR AIFVNGKVQA RKVKAAGAIE LSSTPTKPTP  
 AEASETIATA LAKGGIDL FH FSDKAASLRD RLKFIHEHRG EPWPD IETAD PHLWLSPEIE  
 ALSHGTRLNN IDMYPALQRL LPWPEATNFE EFAPSHLSVP SGNQHRLDYS SGRP VIRVKL  
 QECFGLEESP QLCGIPVQFH LLSPAGRPLA VTDDLRSFWS GPYSQVRAEM RGRYPKHPWP  
 EDPWTAPATA RTKNRM

> RXA02357 (1-1203, translated) 401 residues  
 NSSRPEEITD LSAVPDWTF L EKR PENTLGS QLELRFVML RRALKNRHAK LVDRVNGSNS

YVDIEMSSGV RWRMSEQVDR GYTRPDFWFE PLNGNYPTVA VFTDGAAFIH SSANYRLDGD  
 IQKRMKLALD PDNLPWNIT SLDLDRFSNP AAQGEPAWF SPIGRQLSKA NLILDQSTA  
 LLAATPMDQL LAFLDNPAAS SWKEFAHIAA AHMLGHNPK NGDGIVGTFR NKISLRATMV  
 NRELARQLW LAPTTPEELE VDTWTAFLNL ANLMWLAPES VYVSTNGSPH KIDIVPAPAA  
 PLVVEVPELW APILDGFTAD EDEEAEGALQ ILAKEHALVP ETTGDELSSI PTIATWPSVK  
 IALLYESDPD EPLEDDLKAE GTWLLFANDL ETSDIPAALR P

> RXA02359 (1-1869, translated) 623 residues

VELPSPGEAL AHAGHTPEVL EAELGIDPAA TRIVLELASE DDIAAALPSS PTWEKDALIG  
 LVAGLSIEDI RESLAIPAPS TEPDTRSEDIT RLIAGLKTPA AQMDFAYLDT PNSNDLRRVI  
 ETEGFDSDRV YIDPSQSLV TRNFSGSGRV FGGAGTGKTV VVVHRANRLV TSDGHLETDD  
 KTRPVLLTTY TRGLADALKS SMNALNPFTF EAEKPGSPGL WISGIDALAN KVVALANTAE  
 REAATTAILG RAAGRITPFI GNGEQEFWID AIISADPGDL SEEISNTEFL AQEFETVILA  
 RGITQEKDYL RAPRPGRGTP LNRVQRKKVW AIIQQFMTSC AREGKMSWPA LSSIAANILE  
 QRAAAGQGRF FDHVLIDEAQ DFHAGHWLLL RAAVAEGPND IFLAEDSHQR IYQHHVLSR  
 FGISTRGRAS KRLTLNYRTT AENLSYALGM LTGEWTDAG ETDTIEHYRS ARKGPKPHLY  
 QFESETDEFE AIAELIKVWQ DRTTDVRIGI LARTRPLINR VVNALSEQGI DAVKTQNAEL  
 AAHETVSVMT MHGAKGMEFT HVILIGMGRD LIPLQYTMQG LGEAERNDQA QRERSLLYVA  
 ASRARDALVL THTPESELL PRV

> RXA02363 (1-4800, translated) 1600 residues

MSNAPKKSFS DFFSPLATET ETTITLSAIE VEKVNKTEV TRNIDPVEAA EQISRDRYRRY  
 LKTLISPSNK TIAAEFNREI DESENLYVGP ILQLTPPYAP GKSPAQLIDE GVLSPNFSRL  
 DAALPKDRPL YQHQEDALRK IASGRNLIVS TGTGSGKTES FLIPIFDQLL RQQQAGELNP  
 GVRALLLYPM NALANDQEKRL RELLEADTPE ITFGRYTGDT KQTREEAEKY FKLINGRNAT  
 PLPNELISRD EMQENPPHIL LTNYAMLEYL LLRPADNAFF DDAYSNWKF LVLDEAHVYA  
 GAQGTEVGML MRRLKDRVQR GNPLQCIATS ASLEGTKEAI MTFGQDLFGE PFEFVNEDPS  
 RQDLVSAHRR KLPKFTFTWSL PDELFDQPLE SDGLFQALQE RGGDQYEELS KEEHIVKLRE  
 LSQSSSTRVE DIGKGLWPNV TDKASMRTH MLVNLGSGVL SHDGVPAISA RYHMFVRAVE  
 GAFLGYTEQG KPIVSLDRQV TLGDTARPMY EMGACIKCGT VHISAHNDSD FLVPPENSSN  
 FDEQQLKWV LTDDFETADI DEDDLETDAD ENVKVLELQK LCTACGKLNG KNSLLCSGCS  
 SHHDQFIDVK ILEPRNGSQL TCTRCGGREK NLIRRLRTDS NAAPSVLTTS LFQLLPESAD  
 QDTSRKIGAG RKLLTFSDSR QAAAYAAPYL QASYTRLER RILIELRDE EFTEGASIER  
 WISRASEVAK NNRVLANNLN PRETLEQTGN WVFDLASTV RSSSTEGGL AKIELTPEAL  
 SQLSFRKPLG EMFGDPDAAD AFFNLFAQEF RHKGAINCPD YVNLEDERFG PRRGQHFFTK  
 DGGRKSTRRL YSWIPQRGTN NRKDFITKVL NRIGQAGDEG ENITTLHLHL WNDYTNSEIL  
 KVPGEKAEGY TLNYSNLQVS PGKQHSWYEC DTCRNTTFFN VLGLCPHGFC KGKLKEIDTF  
 LPEYATNHYR KLATSLEILP LSAKEHTAQW TPTEAAEVQK EFIEGKINVL SCSTTFELGV  
 DVGDLQSVMM RNVPRTANY VQRAGRARR SGSAFVLTF AKRSSHDLAV FKNPTQMDIG  
 EMTVPFLHIN NARIARRHTY SIALAAFFRE QAAQNRFWKK AGEFFLGTD APLYRPAVAE  
 QEATEILEEF LSPVPNYITE ALRRVPFESL HEDLDIENQG WVKQFLEIFD TTRQEISEDF  
 QTLKKMQGRA LGSEQGKAD AFKRTITTLM QDQLLGYLAK KNMLPKYSFP VTDVLDQTNF  
 SEAGNKVSL RDLQLAITDY APGAELVAGG KLWKSAGIRH LAGKKVETFY WTTCTECKHT  
 ETSRFGFTSE DVCSQCSAPI SLGKENKFLI PRFGFVADPN PTEVGTAPPV RSSNRLEFVK  
 QFGVKDDSEE FSNSDGTATA QVLTSSWSRT EMGALETGPN KNGFWYCQC GFGTPNGAEI  
 PKSHRNPRTK QCGTYYLEP HSLGHTYQTD IATVAVPSYT NLDFEGWRS MYAIEAAAE  
 CLEINRDDLN GTMAKHDRNP TMVLFDTVPG GAGITRKVRE NFPQVLEAAI RRVETCSGCI  
 DTSCYACLRS FSNQRFHLDL RRDIALDLLH HMAVAMPKSE

> RXA02369 (1-2289, translated) 763 residues

VPNNKAVEAE ISPSAVLAAE FDRDSLSEKT RVHQLAKRLG MVSKDVVAL DGIGLVKVAQ  
 SNLSKEEVEK LLDALSQPVL NAAPAAVPDV EPVEKIRRRV EKNVENEIHQ IEEKVERELA  
 AVAQPTDFEA AAREEATAEL LEDIVPEITP APVEASVYTP IFVAPAVVPT ENVQDDEQ  
 VRERTARKRR GRRGTGRGRG AEAETVTEVS EEASTSEVEE VNEPIGIGKS TRLEAQRARR  
 TEMREENKKR RHVSTQEFM ERRESMERRM IVRERQRHDH PGLVTQVGVL EDDQLVEQFV  
 TSDAQMSMVG NIYLGRVQNV LPSMEAFAID IGKGRNGVLY AGEVDWKAAG LGGRGRIEQ  
 ALKAGDQVLV QVSKDPLGHK GARLTQISL AGRYLVVYVPG GRSAGISRKL PGPERKRLKE  
 ILGRVPAQG GTIIRTAAG VSEENIAADV NRLHTLWEQI KERTAEKKKS RSKPITMYE  
 EPDMLVKVIR IVDNEDFTSL IVDGDRWNT VRAYIQSVAP DLVSRVEHFN RADFDGKDAF  
 EAFDLNTQLE EALSARKVNL SGGSLIIDRT EAMTVIDVNT GRYTGKGGGN LEETVTLNNI  
 EAAEEIVRQM RLRDLGGMIV VDFIDMVLPE NQELVLRRLN EALENDRTRH QVSEVTSGLG



VQMTKRKIGA GLLETFSSPC EHCEGRGIIV HVDPVDTVDE RVEAKAEERS RRHQRSNSTN  
KAAAEHPMVV AMRDLVESDE HDLDQEFEEEL AASMIVLDDS DLL

> RXA02370 (1-792, translated) 264 residues  
MTPIYYDVND DKLDEPERIL AESTVEPEEG PRMRARRQRQ ESAADDIAAI AAAAVDIASE  
EDPDEPSGSS YVSDFEAEPI APVVEKAAEP VAEPTADYEK ARAEFEASPR RRRKTRGNSR  
SDHAPKPEDF APVVEEVAET PVKTPARKAP RRNRPSSELSS GAPSSAPSTR NRRRAVRRQL  
VEAPETVVEI APEAAPEQVA EPQVEFDQPD NRRKRRRAVR VTAAPVEKKV ASTSNARAPK  
KEPQAASTTN PGRRRRATR GPRS

> RXA02371 (1-270, translated) 90 residues  
MYAIVKTGGK QYKVAEGDLV KVEKIEGEPG ASVALTPVLL VDGADVTTAA DKLASVSVNT  
EIVEHTKGPK IKILKYKNKT GYKKRQGHRO

> RXA02389 (1-261, translated) 87 residues  
MANIKSQIKR NKTNEKARLR NQAVRSVRT EIRKFNAIE AGDKDAAQAQ LRTASRALDK  
AVTKGVFHIN NAANKKSMA TAFNKL

> RXA02419 (1-192, translated) 64 residues  
MKNKTHKGTA KRVKVTGSGK LVREQANRRH LLEGKSSTRT RRLKGIVEVD KADTKRMKRL  
LGKA

> RXA02420 (1-381, translated) 127 residues  
VARVKRSVNA KKKRREILKS AKGYRGQSR LYRKAKEQWL HSMTYSYRDR RARKSEFRKL  
WIQRINAAAR MNGITYNRLI QGLRLAEIEV DRKILADLAV NDFATFSAIC EAKAALPED  
VNAPKAA

> RXA02463 (1-114, translated) 38 residues  
MTYVHCXGRT GRAGHNGTAV TLVGFXETXK WTXDXNEX

> RXA02468 (1-531, translated) 177 residues  
VEITDALEAL GINRTFAIQE YTLPIALDGH DFIGQARTGM GKTYGFGVPL LDRVFDSDV  
AETDGTPLAL VIVPTRELAV QVGDDLQRAA TNLPLKIFTF YGGTPYEEQI DALKVGVDV  
VGTPGRLDL HKRGALSLEK VAILVLDEAD EMLDLGFLPD IEKILRALTH QHQTMLF

> RXA02522 (1-543, translated) 181 residues  
MWARDINFLY MSTEQELQIG KVVKSHGIRG EVVVELSTDD PDIRFAIGEY LNGKQAGKEH  
SLTIDAARMH QGRLLVKFAE VPDRTAADSL RGTRFFAAPL EDEDEDGFI DHELEGLRVI  
HEGEDIGEVT GVMHGPAGEI LEVRLTSGKE TLIPFVHAIV PEVDLEEGTA TITPPEGLLD  
L

> RXA02533 (1-567, translated) 189 residues  
MEDDLAALV KALFDARTQR RLSISALAES SGVSRAMISR VENAEAQPSA ALLGRLSGAL  
GMTLSELIAQ AEGGYDRGAR RSKQSVWTD ATGYTRRAVS QPSESPLLV EVMLPPGAEV  
GYPADAYRFM DQVVWVLEGA VRITEGEEVH ELSTGDCLRF GPPRDTDFAN PTTVATRYLV  
ALDKRVPRA

> RXA02615 (1-636, translated) 212 residues  
MQFAQNPRLT NDAVILEPLS HQWTQDLQEA VASQELWRHW FVALPTPEGM AEEIDRRLA  
HADGLCAPWA IISAATGRAV GMTSFHTLDH ANKRLEIGRT WMAAHVQGTG INPSVKFLQL  
QRAFEDLGVN AVEFRTNWHN HRSRAIERL GAKQDGVLRK HRIHPDGTVR DTVIYSITND  
EWPVAVKLTLM ERLYRHMVQV IIPNEASLFD AS

> RXA02633 (1-264, translated) 88 residues  
MKKDIHPDYH AVVFQDAGTG FQFLTKSTAS SDRTVSWEDG NEYPLIVVDV TSESHFWTG  
AQRVMDTAGR VEKFERFFGG MARRKKKA

> RXA02635 (1-234, translated) 78 residues  
MSAHCQVTGR KPSFGKSVSH SHRRTSRRWN PNVQRRKFYV PSEGRITILT VSTKGLKVID  
RDGIEAVVAQ IRARGEKI

> RXA02636 (1-162, translated) 54 residues  
MARNDIRPII KLKSTAGTGY TYVTRKNKRN NPDRISLMKY DPVVRKHVEF REER

> RXA02637 (1-303, translated) 101 residues  
MAKKSKIAKN EKRKEIVARY AERRAELKAI ISNPNTSDED RLDAQFELNS QPRDAAAVRV  
RNRDSDHGRP RGYLRKFGLS RVRMREMAHR GELPGVRKSS W

> RXA02657 (1-3582, translated) 1194 residues  
MARLSHMAKQ SSFVHLHNHT EFSMLDGMK IDMLADEVKA QGMPAVGITD HGNMYGSNPF  
YRKMTEMGIK PIIGIETYMA PESRFKKERV RWGEPHQKSD DVSGSGAYLH QTMLAENTTG  
LRNLFYLSSM ASYEGQLGKW PRMDADIIE HAEGIIATTG CPDGDVQTRL RLGQFDEALE  
AAAMWQDIYG RDNYFLELMD HGLDIETVR SELLEIGRKL NLPLVTNDC HYVLESQAQA  
HEAMLCVQTG KTLHDEDRFK FGGTGYVKS AEQMRALWDD MVDGCDNTL WIAERVQSYD  
EIWEHSHDR MPIADVPEGY TPTTWLHHEV MAGLEDRFSG QQVPEDYIER AEYEISVIDM  
KGYPSYFLIV AEIHKHARS GIRVGPGRGS AAGALVAYAL TITNIDPMEH GLLFERFLNP  
ERPSAPDIDI DFDDRRRGEM IRYAADRWGE DKIAQVITFG TVKTKQALKD SARVQMGQPG  
YQIADRVIKE LPPAIMAKDI PLSGITDPDH PRFNEAGAVR QLIETDPDVK RIYDTARGLE  
GVVRQSGVHA CAVIMSSVPL LDCIPMWKRP ADGALITGWD YPACEAIGLL KMDFLGLRNL  
TVIGDAIENI KANRDGEVLD LENLAIEDEE TYKLLGRGET LGVFQLDGGG MQELLKRMQP  
TGFNDIVAAL ALYRPGPMGV NAHWYADRK NGRKPITPIH PELEEALIEI LGETYGLIVY  
QEQIMRISQK VANYTAGQAD GFRKAMGKKK PEVLEKEFAN FEGGMKANGY SDAAIKTLWD  
TILPFAGYAF NKSHAAGYGL VSFWTAYLKA HYAPEYMAAL LTVSGDNKDK SAIYLSDCRH  
LGIIRVLPDI NESSLNPLPV GTDIRYGLA IRNVGAEVVD SILDTRKEKG LFKDFS DYLD  
KIDTLPCNKR ITESLIKGA FDSLGHARKG LMLVFEDAVD SVIATKKAAD KGQFDLFAAF  
DSDNNDDVAS FFQITVPDDE WDRKHELAL REMLGLYVSG HPLDGYEDAI AAQVDTALT  
IVAGELKHGA EVTVGGIISG VDRRFSKKDG SPWAIVTIED HNGASVELLV FNKVYSIVGS  
MIVEDNIILA KAHISIRDDR MSFCDLRLV PELGPGNGQG LPLRLSMRTD QCTMSNIAKL  
KQVLVDNKGE SDVYLNLDIG DNSTVMILGD HLRVNRSASL MGD LKATMGP GILG

> RXA02682 (1-327, translated) 109 residues  
MSYHDHSDIE YLKKIGANSP DAFKAFVHFD EAALRGPNKK IPRNYTEMIA LAVAFTTQCA  
YCIDIHTAAA KKEGVTEEL AEVALIAAAL RAGGAMTHGA LAMKLYDEN

> RXA02752 (1-495, translated) 165 residues  
MAVKIKLQRL GKIRTPHYRV VIADARTKRD GKVIENIGIY EPKAEPSVIK INSERAQHWL  
SVGAQPTAEV AALLKVTGDW QKFKGIEGAE GTLRVAEPPK SKLELFNQAL SEANNNGPTAE  
AITEKKKKAR EDKEAKEAAE KAAAEKAAAA ESEEAPAEAA AAEEA

> RXA02755 (1-1995, translated) 665 residues  
MSAPESPTNT TPDPLNASTE ELLTAAVEAL GGARRAGQEA MAKAVTKAFD TERHLAVQAG  
TGTGKSLAYL VPSIRHAQKS DSTVIIVSTAT IALQRQLVNR DLPRLVDALE PLMERRPTFA  
IMKGRSNLYC MNKVARQEEL NQEDALIEQE DISWLGKHIV RLNEWANETE TGDRDDLDPG  
VPDLAWKQVS VTARECIGAS RCPHGEDCFA EIARGKAKEA DVVVTNHALL AIDALSDVSV  
LPEHDVVVID EAHELDGRIT AVASAEITVN SLNLAARRAS KLDSDKREER VQEIAGDLET  
LLQTMQPGRW NDMDEGSKGT LVALKDALWA LRAQIAGAPE GEAANDPERF AERQNLNHL  
MEIHDANVRI LEVFAEEDPS KQYDVVWHNH DRRGDSLNV APLSVAGLLH EKLFAENTVV  
LASATLTIGG NFNAMAASWG LPKGSWDSMD AGTPFDPAKS GILYTARHLP DPGRDGLPEE  
TLDEIYELIT AAGGRTLGLF SSKRAAEQAT KAMRLRLPFD VLCQGDNTA ALVKKFSOSE  
NTCLFGTLTL WQGVDPVGRS LSLVLIDRIP FPRPDDPLLQ ARKEADAEG RNFMEVAAT  
HAALLMAQGA GRLLRHVGDR GVVAVLDHRL STKRYGGFLR FSMPRFWETT NPETVRAALK  
RLVTK

> RXA02764 (1-2784, translated) 928 residues  
MSEYKPPIPS DPQVRLIKPT SKLRPRSWEG EVSHLVKQGT GLWRVTGEAG SGVSSAVVDT  
VLERIRQWE PSSMLVVATS KEAASRLRQE ISESVAQMDY VSEGPLVRSV HSVAFALIRD  
ASDDDVRLIT GAEQDAVIRE LLRGHADDGR GGWPQEQREG LRMVGFARQL RDFLLRAVER  
GVGPDELVEL GERFERANWV AAGEFLREYK QVMKLSGAHS FSASELVTEA LRGPEPSVKY  
RGVFIDDAQH LDPKSAELVS RFFPEAELAV VAGDPQQSVF RFRGANPDFL TKLSVDHEV  
LKGRRKASTS IVVAETESAH ADLLADTVRR AHLIDGRSWS EIAVIVRSAG MIAPWRTLL  
AAGVPVHISP TDVVLAEQRI VAAMILGLRA LTESLNAIEL EDLLLGPIGG ADPVTLRRL  
RGLRQAEMKM GGQRRRAIEVL RSLLAESDAE MLGFLTREL NLLERVRSVL EAGREALAEH

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GSIEEVLWAL WSATDLSNSL SAISLRGGAS GSQADRDLDA MMALFDAAGD YVERYPSAGV
RSFILHISEQ ELPTGMRERR GAIPEAVEVL TAHATTGREW KRVIVAEVQE GSWPSLGETG
TLLGQEEFVD LVDEGIDPDI IISRSAERLA EERRLFYLAT TRSTESLLVT AVNSPDSDEV
REPSRFLELL SQPIVVLEGE EASAIAPPEE IGHRLLSIPA MVAELRRVFN DPRDPRRKQA
ARQLSRALAE GIPGANPAEW TNLRTPTSTDE ELIKGAVSLS PSRIEQLLNC PLRAVLDRLD
SEEETPIAML KGTLVHAFAE AVAGGVDAAL AEEKVTSAYM QLANVPSWSR ESTEIAFRRI
LSRTDTWLKT SRADFTVGT EMDVSVTIDD SVSIRGRMDR LERNKSGELV VVDFKTGKTQ
IAAKDMGDHP QLFAYQLALS KGV LHGDK

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> RXA02785 (1-3855, translated) 1285 residues

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PVSYPVEDI EVVLDTIATA QHEDDYAQLC FRVFCEKVWL CEADLHAAIS AYAADHLTAA
ILQHAADSTP LSRRDQDEV T ALPELVLGAT ARILGEVKAA EFISHALAAM AFVRAEYGVK
AAWGA KRLPG VETHLVVREV SRIDRALGVG DEQSMFRWSD DGPAEDANTQ QWLPACYCRS
CGRSGWMVSL EQGTNIPVLE EQKIRLNSFE QPHKQALLD ATSEQRAAIE QGRSVAGPRG
VDGTS AVLWF HSASNELSTR QPSPEEQSG SSI AVLTHFG PEADDLSAQ TCPSCGDVDS
IRYIGSGIST LLSVSLSNLF GMADLDSA EK KTLVFADSVQ DAAHRAGYVQ ARSRAFALRT
YTRRAVG DNE VTLPSISRAL MDNATSGRTR YELLPPDLTD LDIYKPYWHP DASKAERREA
SRNVHKRLSF DLALFEGQRA DLPRSLALTG ALSAFVDLPK GVALSAAAEA LYAIEVPTLD
IEDENLRLRW VQGALELLRA RGGINHEWFG AYLRTDGNPY MLNRRQARAE GIPGFVRGGA
PEFPRVGSAL SGSLRSSTGT TPLGSPRGY ASWTSQVLGI STHDAATAIT KLFDALS NRS
ILSSISTDSG GKIYCLEAER IRIFSEDHPE VLECSVCHAQ TGVTDHVRDF LDGAPCFSPS
CGGV LHIEEV EDNYRRLYS AIEPRTVIAR EHTSMLKKKD RLALQSF RG GEGSAKQSPD
APNVLVATPT LEMGIDIGDL STVMLASLPT SVASYVQVRG RAGRLSGNSL VLAVVRGRGV
TLPRNLQPLS MIKGAITPPV AYLSASEILH RQFLAYVIDC LDTRAE LPKL ETAIDVFDNA
AGKTP LVALL KAQIHAGLDP LLEEFVRTLN MQISIDNIFE LRTWASGNST DSSLALLETS
QKEWMEERRS LTARRGELEK IFDKLDARND AHDEELKEEK RKTAASLKAV KLQIRDLLGE
FWIAALERYG LLPNFTLVDD SVELNVA VTS FNPQEV EFD KNHAYSRGIS AALFELAPGA
TFYAQGI AAK VDSIEIGE HG SAIEQWRLCP VCSHSEILQP GVSTPGSCPT CGSPAFADKG
QILEVVQMRK VSSAVEKTRA AISDDREDRF STRFNQHV SF VVPPDGHGKS WYLN DGF GIE
HLPKVELRWL NLGIGNGQKR RLGGFEV TSP LFNVC RHCGH LDSEAGANSR WDHRPWC PHR
YEQKEDTVSF ALGRTLKTQG VLMLLPEYFG SEADSMV VTS LIAAIKLGR EVLGGDPDHL
DVTSVQVPRT SGD GALDALL LHDQV

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> RXA02819 (1-612, translated) 204 residues

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KLQIGDV IAM PGRKRPVLAV VMT PANQSRD PRPWVTTESG WSGRVDAESF TNPPITIGHM
RLPRQAIEEP RRNARRVQEL FRREHFKRPN KMREFARVRP NEAVTKLRNA IRDHEAHHWP
DREHLARTAE RMIRKERDLA KLTGNVDKAR ETLGRTFERI LSLLSEMDYV DYSNPDNPVI
TDEGERLAKI HSEADLLVAQ CLKR

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> RXA02826 (1-399, translated) 133 residues

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MAPKKKKKVT GLIKLQIQAG QANPAPPVGP ELGAHGVNIM EFCKAYNAAT ENQRGNVVPPV
EITVYEDRSF DFKLKTTPAA KLLLKAAGLQ KGSGVPHTQK VGKVSMAQVR EIPATKNEDL
TLAISTLLRR SSL

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> RXA02833 (1-579, translated) 193 residues

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TRVLSLRMGR SFSLAVSVEP EQEIPKPQLK QEFKYQPDAL VFSSNKAPKQ YEVGGRGEAS
TSDGWEGTHS APAPEPH PAP IADREPELAT PQRIPRETPA HNP NREVSLN PKYTFESFVI
GPFNRFANAA AVAVAESP AK AFNPLFISGG SGLGKTHLLH AVGNYAQELQ PGPRIKYVSS
EEYHQRLHQL RAR

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> RXA02883 (1-912, translated) 304 residues

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MSFHITSVNV NGIRA AVKQR SETNLGFLPW LEETRPDVVL LQEV RASEKD TATALQPALD
NGWHYIGAPA AAKGRAGVGI LSRHELEDVN IGFGSFLDSG RYIEATIKDT TLDVPVTVAS
LYLP SG SAGT DKQDEKYRFL DEFEGFLDQR AKERSH MVIG GDWNIC HRRE DLKNWKTNQK
KSGFLPDERA FMDSVFGTFP DEATQVAGAG DFFGAVDYEG TRRREAT TDP AWF DVARRLQ
PEGDGPYTWV TYRGKAFDTG AGWRIDYQAA TAAMLER AER SWVDKAAAYD LRWSDHSPLN
VIYS

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AVAFDVGRKTFRTDMFPAYKAQREATPPEFKGQVEILKEVLSTLGITTIEKIDFEADDVI

ATLSVAAKPLGFKTLIVTGD RDSFQLVNDTTTTVLYPMKGVSVLHRFTPEAVEEKEYGLTPR  
 QYPEFAALRGDPSDNLPNIPGVGEKTATKWIAQYETLDNLLDHADEIKGKVGASLRERIE  
 QVRMNRKLTEMVKDLELPLGPDDFEMKPVQVAEVAAKFDDLEFGTNLRERVLA VVKAEGS  
 AAPVEEVEAEQVVVD TQSLAQWL PARAGQALALALAGVAKPAAGDTYALAIADTKRHA VL  
 VDVADISAEDEKALATWLASEDPKMLHGAKAAYHMLAGRGFELHGVVHDTAIAAYLLRPG  
 QRTYELADVYQRHLQRQLSTNDNGGQLTLLDAADDQSLVDDVIAILELSEELTKQLQEIQ  
 AFELYHDL EIPLSGILARME AIGIAVDVATLEEQLKTFIGQVAQEEEAARELAEDPTLNL  
 SSPKQLQVVL FETFGMPKTKKTKTGYSTAAAEIEALAIKNPHPFLDHL LAHRQYQKMKT T  
 LEGLIREVAPDGRIHTTFNQTVASTGRLSSTDPNLQNI PV RTEAGRKIRSGFVVGE GYET  
 LLTADYSQIEMRVM AHLSDQDPLIEAYREGEDLHNYVGSKVFNVPIDGVTPELRRQVKAM  
 SYGLVYGLSAFGLSQQLSIPAGEAKQIMESYFERFGGVQRYLREIVEEARKAGYTETLFG  
 RRRYLPELTSDNRVARENAERAALNAPIQGTAADI IKVAMIRVDRSLKEAAVKS RVLLQV  
 HDELVEVAAGELEQVREILEREMDNAIKLSVPLEVSAGDGVNWDAAAH

>RXN00066 TRANSLATE of: rxn00066.seq check: 6030 from: 1 to: 813  
 VTDPLSAALDSGRINHAYLFSGPRGCGKTSSARILARSLNLCVEGPTSTPCGVCNCSVALA  
 PGGPGLDVTLELDAASNNGVDDMREL RERANYAPAESRYRVFIIDEAHMISTQGFNALLK  
 IVEEPPAHLIFIFATTEPDKMGITIRSRTHNYPFRLLTPGDMRKVLKNAVDGEGVHDDS  
 VYPLVIRAGGGS PRDLSILDQLIAGSGPEGLTYERALPLLGVTSFTLIDDSIHALASKD  
 NASMFTTIDNVIEEGLEPRRFTIDFLSTRSG

>RXN00103 TRANSLATE of: rxn00103.seq check: 3594 from: 1 to: 4560  
 MAKSI LSRFRPQVAEWF RDVFASPTPVQEGTWEAVSKGKNALVVAPTGS GKT LA AFLWAL  
 DSLTEQTGQQVLD TGTPVPVRGGKVKVLYISPLKALGVDVENNL RAPLTGIARTASRMGL  
 DVPNITVAVRSGDTPSAERARQVRKPPDILITTPESAYLMLTSKAGATLSDVDVVIIDEI  
 HAMAGTKRGVHLALT LERLEKLVGRPVQVRGLSATVRPLETVAGFLGGGRPV EIVAPPAE  
 KKWDLTVTPVEDMSDLPVQEPGSTIGELVMDDPLGITGESALPTQGSIWPHIEQQVYNQ  
 VMSAKSTIVFVNSRRSAERLT SRLNEIWAMEHDPESLSPQLRRDPAQIMSSADVAGKAPQ  
 VIARAHGHSVSKDERATTETMLKEGR LRAVISTSSLELGIDMGAVDLVIQVESPPSVASG  
 LQRVGRAGHTVGATSIGSFYPKHRSDLVQTAVTVQRMKEGLIEEIHVPKNALDVL AQQT V  
 AAVSIKDVQVDEWYETIRKAYPYRDLAREVFDSVIDLVSGVYPSTDFAE LKPRVVYDRVS  
 GVLEGRPGSQRVAVTSGGTIPDRGMFGVFLVGDGPRRVGELDEEMVYESRVGDVFTLGAS  
 SWRIEEITRDQVLVTPAPGHTGRLPFWTGDAAGRPAELGKALGA FRRSTLTDPSSSGLEG  
 WAHDNLIAFLQE QEESTGVLPDEKTLVLERFKDELGDWRIVLHTPYGRGVNAAWALAVGA  
 KIAEETGMDAQAVAGDDGIVLRLPEGDEDP SAALFMFEAEIEITLVTEQVGNSALFASRF  
 RECAARALLPRNRNPGKRAPLWQQQRQAAQLLDVARKYPSFPII LETVRECLQDVYDLPA  
 LKNLIEDLQLRKVRIA EVTTQQPSPFASALLFN YTGAFMYEGDSP LAEKRAAALALDPAL  
 LAKLLGEVELRQLLDPDIIAEVHQQLRRQGDRAARNNEELADSLRILGPIPLDELGEHIT  
 FENPDLED RAMTVRINGREHLAQVLDAPLLRDALGVPVPPGVPAQVETITDALEQLVNRW  
 VTRTRGPFTANDLAEAFGLGIATAITALQSAPVIEGRYRQGV DVQ EYCATEVLSIIRRRSL  
 AAARKQTRPVQS AFARFLLDWQQIAPVGATPELRGVDGTYTVIEQLAGVRLPASAWEDL  
 VLPRRVADYSPIHDELTSNGEVLIVGAGQAGSRDPWISLLPV DYA AQLVGEASTSMSPL  
 QDAVL DQLRAGGAFLFSDILEENFGYT TAQLQEAMWGLVEAGLVSPDSFAPIRARLASGT  
 TAHRAKRRPARSRLRTRTSFASDVPPDMRGRWTL SVQPADATSRSVAHGEGWLD RYGVLT  
 RGSVVAEDIVGGFALAYKVLSGFEESGKAMRGYFIEGLGAAQFSTPAIIDRLRGHDDSPD  
 VEGWP SGATDPD VYLIAAADPANPYGAALPWPEQGPSRAAGAMVVLCDGLLLAHLTRGGR  
 TLTVFSDNIPKIATALITYERLTVEKINGDNVFDSP LLEQFRKHGATITPKGMRFRPPVA  
 RETPSDTLPTRTFRGGFGRR

>RXN00163 TRANSLATE of: rxn00163.seq check: 899 from: 1 to: 618  
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 VTHGTIATIADDSGIAVEELNGMPGVLSARW SGAGHNDTANNELLLAQMEHVPDERRNAA  
 FVSVCVLALPDGQEFVQEGRWEGQLLRGPKGENGFYDPLFIPAE EIDGQRSSAELSAE  
 EKDALSHRQALRGLVEKIAQVAAAS

>RXN00407 TRANSLATE of: rxn00407.seq check: 2077 from: 1 to: 2664  
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 QLRGILSTNPESAARGSVRLAGAKQALARKMPLADAES ELHPMGTTWMRSGDTLLKAHPD  
 YADLIATTVELAAECAFTLDLVAPNLPKWDTPGEHTEMSWLAHLVSTRIDTRYVGRSADI  
 KARAATQIDYELGVIEKLGFPGYFLVVNDLVEFCRDSNILCQGRGSAANS AVCFVLGITN

AEPISAGLLFERFLSPDRDGPPDIDIDIESGRREEVIQYVYEKYGRDNAAQVANVITYRT  
 KGAMRDAARALGYPOGAADAWAKGTSEPPDDVLELAAQFKGQPRHLGIHSGGMVICDRPI  
 ADVVPVEWARMDNRSVVQWDKDDCATAGLVKFDLLGLGMLEAIHHMLDLVAEHRGKKINL  
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 ALWQAGVAATEKPGMLPGLSVIEAPALPGMSAFELMATNISATGVTADYQPMALIRERME  
 ELGIVPADRLLEVEDGTRLRIAGIVTHRQRPQTASGLTFLGMEDETGLMNMVMSVGLWQR  
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>RXN00414 TRANSLATE of: rxn00414.seq check: 6909 from: 1 to: 354  
 MQGEASVPFAELHATSSYNFLTASDPSDVVVQAKKLGLAALSVMDDRGFYGAVRFAEAA  
 AEAGMHTVYGAELSLQEGVLTVLCKNPEGYKKLSHLISDAKMAREKRGSSLSAAANGC

>RXN00460 TRANSLATE of: rxn00460.seq check: 909 from: 1 to: 471  
 MPEHPLHVIFDNVPIPPNTGNAIRMCAGTGAHLHLVEPLGFELTEKHLRRAGLDYHDLAD  
 VTVHATFDEAMAAVPGRVFAFTTTANTRFTDIAFEPGDALLFGTEPTGLPQEHVEHSRIT  
 SELRIPMLPGRRSMNLSNSAAVATYEAWRQLGFVGGV

>RXN00542 TRANSLATE of: rxn00542.seq check: 3719 from: 1 to: 675  
 MAIGDTNITVVGNIADPELRFTPSGAAVANFRIASTPRSFNRQTNQWEDGEALFLTIVNV  
 WRQAAENVAESLSKGMRVIVTGRLLKQRSYETREGEKRSVFEVEADEVGPSLTFKADVQR  
 TPRGGNSGGNYGGGNQGGGLGNGQNGQGGFSNQNSGGFGGNQGNQQQSNQGGFGGNQNG  
 SQGNFNFQGGFGGGSPQAAPDNDPWNAPPAGSGGFGGADDEPPF

>RXN00545 TRANSLATE of: rxn00545.seq check: 1627 from: 1 to: 267  
 MIILDPSQDERTVAPSLDKFLEVVRKDKGDVVVKVDVWVGKRRLAYPIDKKEEGVYAVVDLK  
 CESATVLELDRVLNLNDGVLRTKVLRLDK

>RXN00562 TRANSLATE of: rxn00562.seq check: 810 from: 1 to: 723  
 MDADPLIEDDVSGAEVKDSSDEPLLALTRYVFDGRGPVTRGLFHQVAAILSIVSGSVLS  
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 TYTPLCLIVLEPGTAAWMLGIAWGAIDSVIMNMVWINHPRWLSVLVYLALGWLIVPLVP  
 QLWSGAGPTVVWLLLAGGIVYSVGALVYGFKWPGRNARVIGYHEHFHFIATIVAAIVHLVA  
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>RXN00625 TRANSLATE of: rxn00625.seq check: 6900 from: 1 to: 942  
 GTDEDYIRVAFIYDQTTVKPVGESRIFDDAAFTGTARQPLAQEFQPLNDSEKSFVGVVNH  
 FKSKGSVTRGDADTDGQGNNANVRVAQAQALIDHLENQDDWASKPIFILGDTNSYAKET  
 AMTTLYGAGYTNIAEFDAAGYSYQFSGRIGSLDHALGNEAAMKHVIDAEVWDINADEAIA  
 FEYSRRLNNTSDVFENNVERSSDHDPIKVGFNLSSETTEPTIPVEPTDPAEPTDPTTPVKP  
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 AIALAFQFFHSSN

>RXN00673 TRANSLATE of: rxn00673.seq check: 3349 from: 1 to: 402  
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 QPHNGCRPPKRRRV

>RXN00706 TRANSLATE of: rxn00706.seq check: 3516 from: 1 to: 573  
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 DLTAITGQKPLRRAKKSIAFKLREGMPIGAKVTLRGDRMWEFLDRLLTVALPRIRDFR  
 GLSDQQQFDGHGNYTFGLTEQTMFYEIDVDKIDRPRGMDITVVTAVTDDEGRSLLRELGF  
 PFKGEDGNRQO

>RXN00709 TRANSLATE of: rxn00709.seq check: 7555 from: 1 to: 366  
 VIQQESRLKVADNTGAREILCIRVLGGSTRRFAGIGDVIVATVKEATPGGNVKSIGEIVKA

VIVRTKKETRRADGSYISFDENAAVIIKNDNEPRGTRIFGPVARELREKKFMKIVSLAPE  
VI

>RXN00714 TRANSLATE of: rxn00714.seq check: 3128 from: 1 to: 561  
MATITRTDRLILVPLTVELEDEAHQIYSDSRIWEHRPQARHTNVRVTRDIIKRTNESWGK  
KDLGPGWVYLDRPSEFVGVGGVELIDGKVDLKYRLRPDLWNGYATEISNAATLATKR  
IDDSLPLTARVTTNHPASFRIEKLGLTPVWEGRRVGTEDDPNEPDVRIYSDRPLSDEIL  
EMLKQRP

>RXN00724 TRANSLATE of: rxn00724.seq check: 5366 from: 1 to: 1977  
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GTRALFTGKVKFFRNEPQLSHPEFIVIPDPGSGRRLTATGGMKSLAAYGDVEEVALRLVD  
REYIPIYAGTATMTTWIRIMAAVQRVLETMPVIKEPLSVVPEGMPSFDEAIRGIHDPGHES  
PSTFINRLKYNEALSLATVMAIRRADTKNRKAPPMPRALKGHQHMLIDALNFQLTVGQKQ  
VIREISADIEQVRPMSRLLQGEVSGSKTIVSLIAMLQAIDSGRQCAMLAPTEVLATQHAR  
SLSKTLDDAGLDINVVLLTGSMPTGAKKEALLEIISGDADIVVGTHALIQDTEFFDLGL  
VVVDEQHRFGVEQRDQLRTKGREGTTPHLLVMTATPIPTIAMTVFGDLAVSTLRELPGG  
RRPIQTSVIPDHKPGWVKRGWERIGEVLAGRQAYVVCPRIEGEGGVLEIHAYLSEQVYP  
GLNVGMLHGRMDTDLKDSVMQFEFAQGEIDILVATTVIEVGIDVANATVMLIREAERFGVS  
QIHQLRGRVGRGQHDSLCLLHTTFDEDSPPQGQRLAAISTTTDGFQLSELDLQVRQEGDVL  
GTRQSGSDTKLRHLSFISDQKIERALIDATELVAASRSRALELVSDIAMINQEYLEKS

>RXN00790 TRANSLATE of: rxn00790.seq check: 8140 from: 1 to: 1062  
MSVQLTCPTDIIRNRPTPLKDGDRVIVYGKPAFYAGRGTFSLWVTDIRPVGIGELLARIE  
ELRKRLAAEGLFDPARKKRLPFLPNRVGLITGRGSAERDVLSVAKDRWPEVQFEVINTA  
VQGASAVPEIIIEALRVLDQDPRVDV I IARGGGSVEDLLPFSEEALQRAVAAAQTPVVS  
IGHEPDTPLVDNADLRAATPTDAKRVPDVAERMLINQLRSRSAAALRGWVQREQQA  
LAAIRTRPVLADPMTPINRRRDEIAQAVGLIRRDVTHLVRTEQALVASLRAQVSALGPSA  
TLARGYSVVQVIPRDGSAPEVVTIEQSPPGSQLRIRVADGSITAASMGTOQAN

>RXN00807 TRANSLATE of: rxn00807.seq check: 4862 from: 1 to: 1242  
VFDLAGSKTVSKTLFDAASSARALVRARTTERARARAQHNPAMIHDSGFAQSWLFTGP  
PGSGRSVAAKVFAATLVCSNPDPVVGCGQCEDCRAAMGGSHPDIEHIVPQQLSIGVDAARE  
VIKAAAVSPVAGNWRVVI FENADRLTMAANALLKTVEEPTTESTVMILCAPTTDPRDIAI  
TLRSRCHLYIPTPSIAEVARILVAEGNVSQADAELAAAASGAHIGRARYLAHNNAQRR  
RASILNLAELIFHGDVAFRSVNTLVKVMVETEAKDSNKEKEEGDLEAVRISLGMGAKGKV  
HKAVRGAGDFKALEDQQKLRRTRFLRDSLALVDLAGIYRD A I I ISSQAQVGLTHPDM  
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>RXN00817 TRANSLATE of: rxn00817.seq check: 6901 from: 1 to: 2394  
LTPPDFESEKTQAMRPSFGEELAAIVSKRYSESTLTHMVTLPASKAKYVDWPSWVPASLR  
DALVNRGINKLFSHQEQTALHAWNGQHVVVATGTSSGKSLGYQLPILSALGTDPTACALY  
LPTPKALGSDQLTSTSTLLRDIPDFHPINPAPYDGDTPSEARSGIRDLRSRFVFTNPDMVH  
ASMLANHPRWARLLRHLKFIVIDECHAYRGVFGANVSMVLRLRLRIAIFYGSHPTVILAS  
ATSSDPEIHASRLLGAPVKAVTEDGAPTERTVLLWEPGFIEGAEGENGAPVRRAASTE  
ANIMATLISEGARTLTFVRSRQAEIVALRAQEELSTLGRPDFARRVASRAGYLAEDRR  
RLERLLDDGTLGLGVASTNALELGIDVGGGLDAVVTAGFPGTVASFWQQAGRAGRRGQGS  
VLVARDEPMDTYLVHHPAALLEKPVEAAVFDPTNPHVIRGHVYCAAVEKPLTEAEVAAFG  
AQKVVEKLEIEGLLRKRPRGWFAVEKPMSEDPDELSPDSAHQQVSLRGGSGSEFMIVDIT  
DGRLLGTIDSAMQSQTHPGAVYLHQGESFVIDELDLEENLALARPDPDYTTYARSDTD  
IRITSAPLEDEVFDAGGGLWVANVEVQVTDRTVGYVTRLSDGTTLDATPLYLPQILQTR  
AVAYTIDPLALEAMGIPAADIPGALHAAEHAAIGMLPLLATCDRWDIGGVSTALHADTGY  
PTVFVYDGMGGAGFADTGFRFAQWIEATFEVVRSCSCSGCPCSCVQSPKCGNGNNPLD  
KAGAIKLLGAMVTLLGTS

>RXN00890 TRANSLATE of: rxn00890.seq check: 1452 from: 1 to: 1299  
LSIATVVALLFSGLLGAVESALSSVSRARVEQMLKDEASGSASLLRVIDERALHINMLIM  
LRTLLDASAAVFAGAIAVNVMSWANGIVLAIVVVSLLTFAVVGVFGRVGRKNPYSVML  
RSVAVLSGLAKILGPIARGLIWIGNIIAPGPGFRNGPYATEVELREMVDIAQEHGIVEIE  
ERRMIQSVFDLASTTVRQVMVPRPEMIWIESGKTAGQATALCVRSRHSRIPIVIGENVDDI

IGIVYLKDLVQKTTYATDGGKSVLVDEVMREATFVPDSKSLDALLQEMQEDHKHIAILVD  
EYGGVAGLISIEDILEEIVGEIADAYDAREVAPIEKIGDRTYRVVSRLSLEDLKDHIIEE  
LDLEIEFGDEIEDQVDTVGGGLIAFELGRVPLPGATVETCGLKLTAEGAKNRRGRRLMHSA  
VVEVGEPSEDNEG

>RXN00897 TRANSLATE of: rxn00897.seq check: 6537 from: 1 to: 1005  
MTPSLPRFRSQKPAVGDRVVARRRIPGANVHWDVIGHVIGVDPLVVRPQSVGGMPSDAE  
EIVIPDDQLEVIKILSPRTIRNSDIRAVEVATAKAFPLVNEWDGWLRLRAGDGIASRN  
SASPLGPSVSGSEPPMEDISRFYARHDLPVKLHPIERIGRPAQKVIDADPQKWVMGPEIL  
VMTKSLDHVESHELPGGLEFSVDKQPDQEWLGMVHFRGQALPAHALELLRTQIEGRMGFG  
RLTTPAGQTVAITRATITAAEERIFLGYSAVEVDPAFRROGLGTALGSRIQEWGAEQHAQ  
EAYLQVVAHNEAGIGLYQKLGSEHHRHRYAERKF

>RXN00990 TRANSLATE of: rxn00990.seq check: 3149 from: 1 to: 465  
IPVLVATDIAARGIDVDDVSLVVHVDPPAEHKAYLHRAGRTARAGTSGTVVTLVMDEQIK  
EVRELFQKAGVTAAEVKVNENSPELAKITGARRPSGVALPAPGQQQPKREQKNTHNRSDS  
RGSSRNPRRRQSGSRSTGRSNPRRQTSRKDGPKS

>RXN00994 TRANSLATE of: rxn00994.seq check: 7403 from: 1 to: 351  
MTTFLELKLDPDEIVRELRSQGITAEAFPIQEAAIPDALAGKDVLRGPTGSGKTFTFGLPM  
ITRLARSGASKPGRPRGLVLVPTRELAAQVRERLDDPARVMGLRVLEVVGGNINRN

>RXN01030 TRANSLATE of: rxn01030.seq check: 392 from: 1 to: 1176  
MTSTTQPGTTPPELSADTHSEPWDVIENTLEPFQKVVRQFIIDRPYSGIFLTMGGGKTLT  
TSLALTYIQPPGHILVVAPLNISRLTWPEEVRKWNIPVNAISLITNERGKTLTRAKRLKL  
YEETATTPPTLYITINLLEDIVNYFGDRWPFWTVIDESQTISDISSKRTRALFVSVPY  
IGRLILLTGTPSANKFDSIYAQVAVLDYGASLGDNIDVFRARWCAPDIITDKQVRRWKPA  
NKQAEAEVYRTISHLVMSAVNTDIKLPPLHFVDHEVHMSDDEHRDYELFKKDAVLAALLD  
MAEENEGGEGADDDAADSATTPPASSQPTNPAIPAGLLQAIQQTQDTNGRAIAPVTTA  
ELDHFDLDPVQRQEDLGTLLVVISAVHASDSAA

>RXN01066 TRANSLATE of: rxn01066.seq check: 7389 from: 1 to: 726  
MRRDSFRDRALVVKTYDFGEADRIIVLLTRDHGIVRGVAKGVRRSKSRFGSRLQLFVELD  
VQLYPGRKLSTISGADTVGYASGIIEDFTRYSCASAILEIATHIAGLENDPHLFEETTR  
ALKNIQDSPEPILNLDEFMLRAMNHAGWAPSLFDCAACGRPGPHNAFHHPGVGGAVCLYCR  
PPGSAEVPPEALHMMWLAVANGQAARIPREHPEQQTTHQLTTAHLQWHIERKLPTLAVLD  
QA

>RXN01343 TRANSLATE of: rxn01343.seq check: 8146 from: 1 to: 708  
MSKNSKAYREAAEKIDAGRIYSPLAANLVKETSSKNYDASIDVAIRLGVDPRKADQLVR  
GTVSLPNGTGKTVRVAVFAQGEKATEAEAAGADFGTDELVEKIQGGWTDVDAIATPDQ  
MAKIGRIARVLGPRGLMPNPKTGTVTNDVAKAIEEVKGGKISFRVDKASNLHAAIGKASF  
DAKKLAENYGALLDEIIRIKPSSAKGIYVKRVTLSTTGPGVEVDTHVTKNYAEEA

>RXN01374 TRANSLATE of: rxn01374.seq check: 3251 from: 1 to: 1242  
MSESGALSSTDLSLPGVTIEVRDEIWLTVHTRSTDGFRVKARGLSDYVRDHEATFFETAL  
DKDLKVIDPTQVTVSLDDSSNYRRTRLWLEATMRKTPVPLYQESLSVADQMLADPLEYQL  
AAVRKTLSSANLRPRVLIADAVGLGKTLEMGMILAEIIRRGGERILVVTPRHIMEQFQQ  
EMWTRFAIPLVRLDSVGIQQVRQKLPASRNPFYFPRVIVSMDTLKSPKYRAQLEKVHWD  
AVVIDEIHNATNAGTQNNELAGTLGPTAEALILASATPHNGDPESFKEILRLLDPTAVMP  
DGTIDAEAAQRLIIRRHNSPEVSGFVGEKWAPRNEPQNFLVAASKEENGVAALNHVWI  
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>RXN01378 TRANSLATE of: rxn01378.seq check: 4647 from: 1 to: 1755  
VKAFLSSPAALGETVSNRLKKASAPEEKRAETLSQLNSAITPQTSQKYQSLLSYLGDIG  
VKKNSDTRVVFISERVATLHWLQENLIRDLKMPPNSIAVMHGGLPDQEQMRLVDEFKKT  
SPIRIMITGDVASEGVNLHTLCHNLVHYDIPWSLIRIQQRNGRIDRYGQTHNPSIVTFL  
DPAEDSKVGEVHVLERLMEREHEAHSLLGDAASLMGKHSEERLEEETIREVLGAQNFNDA  
VADPAEVLNPAGLDDIDWLLAQIAQADAKAETEAEETENQTAPDAASNSTQHAQRRLY

AQESSFLYDCLEGGFNNVPEDSINRGGVGFKKHDNDIVELTPTDDLRRRLDFLPQDYVAA  
RKVKEDLLLASTLMRGQERLNAARTGEDGSTWPSAHYLGPLHPVTSWAADRALATMPRSE  
IPAASGKVTEPTVLLMSTLSNRRGQIVSRFVASSGPFDEVLSDPIQWLHSIGLDETAI  
NPGTAALPDDIEQLISLAVQAARGEIRPLMIAARAQAQTRVEHWAKRAEAWNNKRSGAAS  
TSRTARTAKLIEEQKLSNALEPDRELIRPLAVILPQPATLNTEV

>RXN01380 TRANSLATE of: rxn01380.seq check: 8341 from: 1 to: 2199  
LDEGNTVPFIARYRKEITGGDDTQLRDLEERLSYLRELEDRKQSILAAIEEQKLTDDL  
RSLILGCDTKARLEDLYLPFKKRRKTKADIAREAGLEGLVDKLIIDAPSLDAAAQAAFTT  
EGFEDSKKVLGDGARAILIDRFALDADLVGEVREQMYRAGSMAASVVAGKEQEGAKFKDYF  
EFSEPFDKLPISHRILALLRGGENEGLVSLNLDAGDDIIYEGLIADRFSLDTHTSWLAEEAV  
RWGWRTKLYVSSGLDVRMRLKEKAEAGALDVFATNLRDVLAAAPAGQSTIGLDPGFRNG  
VKVAVVDSTGKDVATTIVYPHQPNRWKEAVSELANLCATHGVELMAIGNGTASRETEKL  
AGEVADMIKAAGGTRPTPVVSESASVYSASPIAAEEFPDMDVSLRGAVSIARRLQDPL  
AELVKIEPKAIGVGQYQHDVNQVALAKTLDGVVEDAVNAVGVNLTASAPLLTRVAGVTS  
TLANNIVAYRNENGGSRRKELNKVPRLGPKAFEQCAGFLRISGSTDPLDASAVHPEAYP  
VVRNIAKATGLDVSGLIGNSAVLTKLKPADFADERFGIPTVTDI AELDKPGRDPRPEFK  
TASFKEGVEKISDLTPGMILEGTVTNVAAFAGFVDVGVRDGLVHVSAMSDKFISNPHEV  
VRSGEVVKVMEVDVDRKRIGLSRLTDEPGAPAPQKGRNRPAPQQRAPQKQSAKPATG  
SMADALRRAGLGG

>RXN01389 TRANSLATE of: rxn01389.seq check: 5202 from: 1 to: 684  
QDGDKLGRHGNKGVVGKILPQKDMFPLPDGTPVDIILNTHGVPRRMNIGQVLETHLGLW  
ASAGWSVPDPENAEVLKTLPADLLEVPAGSLTATPVFDGASNEELAGLLANSRPNRDG  
DVMVNADGKATLIDGRSGEPYPYPVSIGYMYMLKLHHLVDEKIHARSTGPYSMITQQPLG  
GKAQFGGQRFGEVWAMQAYGAAYTLQELLXXXXXXXXXXXXXXXXXXXX

>RXN01563 TRANSLATE of: rxn01563.seq check: 3710 from: 1 to: 1209  
MVSDDLQPRDGIPPLLSTPGEFTAAADLLASGTGPFADITERASGFYDDRAFLIQIRRR  
GSGTLLFDPEQFRPELTQALKPVLNGQEWIIHAASDLPALWDLHPGLLFDTELARGL  
AGFDHVNLAAMVEQIFDLHLLKGHRSEDWSKRPLPESWLNLYAALDVEMLLELADVMAEIL  
DQQGKLPWAEQEFVHIVDQFATMTEPSETSWQDLKGLSTLKRPDQLVVAREMWLERDSFA  
ASRD LAPGKVL SNK VIVEVARVLPRTPAELA QVKGFPGRSQGATKRWFRIITRAKSPRR  
NWPKPQQRKDGIPDRRAWASYYP EEHEVLQEIRALIDDLAADINVPGENILQPSTLRVAV  
WMAKHTGEIHNAETLNAVLRDYGARQWQIDQTFPILSANLLKL

>RXN01575 TRANSLATE of: rxn01575.seq check: 4786 from: 1 to: 1020  
MKSIDLEQLAGTQSRITYQSRKITDEMVARPVHVAIALWEVPWESAKSGKIEGWVIAVDSP  
RGRFVRSQGTKNQDAVNRTVSMKLSALKGVGRKAWIVTGRRQAALRAALVRENLYVTGSF  
AEQNRAQVKASAISSRAEQSALYKAKKIGFEAERAPRVKERQEAHWWPRLSRTQGTAGVL  
RLATDASTDGVFRGAMCFVASNGDYLLETQDTTASSDELELESITHALIYKLTIGATQAI  
IESDSKAALAEIDFILNNRPRRGRWRGITACARNRFRDAWEALIDDCVVELSRVLGHAGD  
PLNQAADQIAYMGMRAVIFEQKSAHPTLLKGIDKALRKA

>RXN01594 TRANSLATE of: rxn01594.seq check: 4466 from: 1 to: 819  
MVARRRLDAELVRRKIARSREHAVEMIRGRVVFVAGMLALKPATVVEPEVSIRVEEDASE  
DWASRGAKLLGALESFEPLGLKVKGRRVLDAGASTGGFTDVLRRREASEVVAVDVGYGQ  
LIWRLQNDDRVRVVDRTNIRYMTLEDTGGECDMMVGDLSFISLKLTLPAIAKVLSDGADL  
LPMVKPQFEVGKDRLGSGGVVRSPELRAEVTADVAKFAATLGLSLKHVVASPLPGPSGNV  
EYFLWLVDGSGASMPDDQQLSAMIDTAVKEGPQ

>RXN01606 TRANSLATE of: rxn01606.seq check: 3298 from: 1 to: 2676  
MAESNAMDRAQISALLDRAQHTINLAEQANNVRLLLKTPGTATVGDNGTLGTDTYLIPSR  
NITWPDNLYVNVFLDGMNAEATLT DYVASVASIPRLCQIINEGQGGMFRRLFNPTKVQAG  
DQAVFDLMVKLDEISSTHEVSRMLEGVHAARTRQQQGVAFPGIHGVGERYIERAQQVL  
ASALGIAGFGAEPWDGHTLAQARRVVQRYAQDPNSEYRLKSEA EKHLTSINELRVQILLE  
QLPVDALRMATDHRLRFGSLDSIHVATVADV LKTHTSILT TVQGIGAQTAGRMKAAAETL  
KQEALRRQNTSIGDEPTQ PAMRLINVLARFDQTETITPEERARRTRVIDYVEHIPPSLDP  
YIVINPATPEFNNFTDDL RWIDANPNLFHPQTITTPADIWDDYISRPAHYQGLLATLLG  
RDIEGADELLDATT LQKIRDLTLDKTHLTDLHLRGYQSFGARFAIIQKKTLLGDDMGLGK



TVQALSAAHAAATEKDFRTLTVVPASVIVNWTRECKRFLNLPVFIAHGDNKQDAINAW  
 NTNGIAICTYDGVRTMDIPAPGLVIADAEHLIKNPSTKRTQALRKLIDAAPYTLLMTGTP  
 LENKVEEFVNLVRYIQPELITRGMKMQAENFRERIAAPAYLRRNQADVLDLPERTDSID  
 WIDLTPEDRSAYDDQVRQGSWMGMRRSAMLSPTRPRLTSAKMQRILELFEEAAEEHGRKALI  
 FTYFLDVLDELEKHLGERVIGRISGDVPATKRQLLDALSHSKPGSALIAQITAGGVGLN  
 IQSASLCIICEPQVKPTIEQQAVARVHRMGQTATVQVHRLIGDETADERMLEILAGKTHV  
 FDVYARLSETAEIPDAVDITESQLAARVIDEERARLGLTESTGPKDEETALS

>RXN01637 TRANSLATE of: rxn01637.seq check: 3317 from: 1 to: 663  
 MVNSGLDDMRGATSPRLLLEILCARLLASNTVAGPAVSSSTDAAPAATPGGLTGIAAAR  
 AKAREYGQKKAAPAPAPTPEPEVREQSLAPTPEPTPAAEPTSQPAPEPEPAREPVVEVR  
 EASVEKQPASSDPLETIRSRWSELNIVEKQSVRTSIMLTEARVLGLRGDTLVLGHSTGA  
 LAARLNAADHNGILVKVLAEEETGLQLKVECIVGTNPAAEAGF

>RXN01683 TRANSLATE of: rxn01683.seq check: 9344 from: 1 to: 2568  
 VSDDNTGQFDRVNPIDINEEQSSYIDYAMSVIVGRALPEVRDGLKPVHRRVLYAMFDNG  
 YRPDRSYVKSAPKPVADTMGNFHPHGDIAIYDTLVRMAQPWSMRYPLVDGQGNFGSRGNDG  
 PAAMRYTECRMTPLAMEMVRDIRENTVNFSPNYDGKLTLPDVLPSRVPNLLMNGSGGIAV  
 GMATNIPPHNLNELADAI FWLLENPDAAESEAECMKFVKGPDPFPTAGLIIGDKGIHDA  
 YTTGRGSIRMRGVTSIEEEGNRTVIVITELPYQVNPDLNISNIAEQVRDGKLVGISKIED  
 ESSDRVGMRIVVTLKRDAVARVVLNNLFKHSQQLQANFGANMLSIVDGVPRTLRLDQMLRY  
 YVAHQIEVIVRRTQYRLDKAEERAHLRLGLVKALDMLDEVIALIRRSPTPDEARTGLMSL  
 LDVDEAQADAILAMQLRRLAALERQKI IDELAIEIELEIADLKAILASPERQRTIVRDELT  
 EIVEKYGDERRSQIIAATGDVSEEDLIARENVVITITSTGYAKRTKVDAYKSQKRGGKGV  
 RGAEKQDDIVRHFFVSSTHDWILFFTNVGRVYRLKAFELPEASRTARGQHVANLLEFQP  
 GEQIAQVIQLESYNDFPYLVLATAHGRVKKSRLLDYESARSGGLIAINLNEDDRLIGAAL  
 CGEEDDLLLVSEFGQSIRFTADDEQLRPMGRATAGVKGMFRDNDQLLSMSVVRDGEFLL  
 VATSGGYGKRTPLEDYSTQGRGGLGVVTFKYTPKRGRLVSAIAVEEDEIFAITSAGGVV  
 RTEVKQIRPSSRATMGVRLVNLEEGVELLAIDKNVEDQGEASAEAVAKGAVEGPASKTAA  
 EETDSVDNGSDENGEE

>RXN01688 TRANSLATE of: rxn01688.seq check: 5568 from: 1 to: 930  
 QFEGQTKTKLGNTIEIKSFVQRMANEHIGHWLEANPAEAKVIINKAVGSAQARLAARKARD  
 LVRRKSATDLGGLPGKLADCRSKDPEKSELYIVEGDSAGGSAGSGRDSMFQAILPLRGKI  
 LNVEKARLDKVLKNAEVQAIITALGTGIHDEFDINKLRYHKIVLMADADVDGQHIATLLL  
 TLLFRFMPDLVAEGHVYLAQPPPLYKLKWQRGEPGFAYSDEERDEQLNEGLAAGRKINKDD  
 GIQRYKGLGEMNASSELWETTMPTVRILRRVDITDAQRADELFSILMGDDVVARRSFITR  
 NAKDVRFLDI

>RXN01689 TRANSLATE of: rxn01689.seq check: 4148 from: 1 to: 1116  
 VANTEHNYDASSITILEGLEAVRKRPGMYIGSTGPRGLHHLIWEVVDNSVDEAMAGHATK  
 VEVTLLEDGGVQVDDGRGIPVDMHPSGAPTQVQVMTQLHAGGKFDSDSYAVSGGLHGVG  
 ISVVNALSTRVEADIKLHGKHWHYQNFESVPEDELIEGGNARGTGTTIRFWPDAEIFETTE  
 FDFETISRRLQEMAFLNKGLTITLTDNRATDEELELEALAEQGETATELSLDEIDNETEL  
 VEETTDAPKKPKKREKKKIFHYPNGLEDYVHYLNRSKTNIHPSIVSFEAKGDDHEVEVAM  
 QWNSSYKESVHTFANTINTREGGTHEEGFRSALTSMLNRYAREHKLLKEKEANLTGDDCR  
 EGLSAVIFRARW

>RXN01770 TRANSLATE of: rxn01770.seq check: 9268 from: 1 to: 3765  
 MPIIIDNLNSDDSTIGTATEYNPDTDADLLDAINADADLDGATISTNATEEGVDAAAE  
 KPKKKKRKAPALKPKGLTAKFFHRDLTGVGGRGRLNKNVHPTNPDLQSYQPVSDVYTPQSA  
 DHKGIKTRYILTHPTPAVVLSESI SNAFHVSTLRRNNNVNNSDSELAAPYLYQLDIPQL  
 DQMINVADICDYHFHGYNLWVDFTPQTIALRSGKTVLDDGTTASDNTTHVYRVTVHVIA  
 GQDHGSTLLDDQGNQVLDRDDNPISTPSIKRIGAVTDLFDHNPFGFASVNSFAFVDFSWD  
 PATTLVDMNLNDSYLSNHINIASSPTPIALDMVVLNEWSEKSYQLCERVVAQAKLINSN  
 KITAHVSDVIKQNAHNILWFTEQMNP GTTNLSEVPISKKSMLPMSRQLRILEHYDVPLTA  
 YSALFWTVSAIKNESMVQYLVRQNMQLTLSSNLDALNSIVS QLPVPDKDVVAASGYQIQP  
 HFSTQQREAITTDNPLAI IQAGAGTGKSTVILERIEYLCAAGTNPEEIAVLSFTNAAADN  
 ITAKNDKVTSMITISKMVHEIYAHNFPDHEISTIDTIINTLDIEYGDQMVTSYMIQLRDL  
 LYKVMTOGGNANLTALSIFMESHIEAFISVLDQIKQTSLELEIIICYLLLDKLIEPHASP  
 KYLIIDEVQDNSVFVFEFVALRFAAKHNTSLYLVDGSSQTLYEFRSANPKALNSLEASGVF

GTYRLTTNYSRNOEILDFANIHLSDIEANQFAGIQLYANSFDAPTADSFKEKVELDMHHV  
 SKQSEFTDSIPYFMESNKARFDAAILNNEQITIVLAHSGREIRAAQQALAEMYPSITVRNL  
 QSDKGFNNTVFSTFIKDFWFEVTAVDPAHAAFTFTSQVTAHLDKLVRGKREQMEDRVIRS  
 MAAWWRENERDIQGWVQQTQSGAITNEEFFYRLRQCILDYEIRNNRARQSMNLARNNANK  
 EAVAQEKPLLMVSTIHSAGLEFDNVIVLQKPSSDAEMTEEGKRATYVALTRAKKRELI  
 AGSTRAYPRIVTDYEQIVDLLEKRDEERKIKEEEAALATLEAEQETRALAAAEQAQAL  
 LLEHNPLWRDLSDDEEVTALTEQEIINNVEPALQIEEEEEEARALAAAEPAIQYLSQFAF  
 DEFPPDDNVANTVVHVAPQPILHQAVPADVTVQSSTAPVTPVVDLEVTVAADPVEPTI  
 VAAQPEVDDNLVYSTSTPNSHSDVIAVNSDTSENAAVNPVLSDIEALRAIFNNQD

>RXN01772 TRANSLATE of: rxn01772.seq check: 5291 from: 1 to: 4938  
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 MDTGIDLVAYNKDDDAYTAIQCKFYLPPTSLAKGQLDSFFEASGRTFETPEGTRSFNSRL  
 VISTTDKWSSNAEKMLNQTIPNTRIGLSAIAESPIDWDIAYPGSELINLQKEPYSR  
 PHQQTAEIKAEIEGFQTHDRGKLIMACGTGKTFTALRLSEEVARLNGNKARILFLVPSISL  
 LSQTLKEWTAQKTMDLRPVAVCSDSKVSKAAEDIAAYDLEVPVSTDGALIAEKLEHRKRA  
 AGLTVVFSTYQSLPAVHAAQEAGAEPFDLVICDEAHRTTGITLAGEDPSNFTRIHDASYI  
 KAAKRLYMTATPRLFDDSVKGAADHSAEVSSMDDEAIYGPEFHRLGFGAEVEKGLLDY  
 KVVVMTVDEQVAASALTVLGSTPGEELTLDMTSAIIGAWNGLAKRSGKEQDTKTGFSSSD  
 AAMERAVAFARDIKTSQQIAESFPRVVNAYTTELEVKNDDVDEHNLNLSVACQHVGDGSMN  
 ALERNSRLTWLKAPTQSMETKILTNRCLSEGVDVPALDSVIFNPNRNSMVDVVQSVGRV  
 MRKSPGKNYGYIILPVAVPPGVAPSAALNDSRRFKVVWQVLNALRAHDDRFRNAMVNSIAL  
 NEGNIKDLPVETEHTGPTSKDRDNAPYDSAESATQYVLFSLQWQEAITYKLVDKVGTRT  
 YWEDWADDVADIAQAQITRIKALDNASPTIKEEFERFVEGLRGNLINESISDDEAISMLS  
 QHLITAPVFDALFAESSFAKQNPVSQVMQRMADALNSAELNSETEKLEKFYDSVRIRAAE  
 VSSAAGKQAVIKDLYERFFKAFKKQSEALGIVYTPVEIVDFILRAADDVSKKHFGRLS  
 DKDVHVLDPFTGTGTGMVRLQLSGLIKPEDLARKYANELHATEIMLLAYYVAAVNIETTY  
 FGLEGERALRNGEDAPVYEPFDGIVLGDTFQMYEDDDKLDLDVFTANNDRMERQRLTPVQ  
 VIVGNPPYSVGQSSANDNNANLKYPTLDRRIEDSYAKYSTATNKNLSYDYLRAFRWATD  
 RIHTQGVAFAVSNNGWVDGNTADGVRLSLAQDFSEIYVFNLRGNSRTGGDLAKREGGNVF  
 NVRVGTQIIIVAVKNPQLSGCRILYKDIDGNLSADAKLNEIAVATIEGAEWQTISPNEYGD  
 WISQRSVDFDTWVVLGDKKNSALKVFQTFAGLKTGRDAWCYGPSTSAQVKTNITRLLET  
 YEQAQRFNSWVVDNGVTSPEKADVQFLKQNPDLADSKISWDSNLKMSLSRGDTFSFD  
 PSSIQMSLYRPFPPQQTYFHVSLNQRRYQLPSMFPTPEHDNQGFYIVNPGSAKPFSTLAT  
 NLLPDLAMWGSNAGQFFTRWTWEPIETREGELDFGNGLFSTTPKKGVEGEILDGYRRVDN  
 ITDEILKLYQSSLGEDVTKDDIFYFVYAQLHDPAYREAYAADLKKMLPHIETPTDRARFD  
 HFVTAGKELMDLHINYEDVEPWDVEVKVEKADPTDRETWRVTMKMWAKVRDPETKKLVE  
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 NPRYIVELIAKVTRVAVETMRIVEEL

>RXN01786 TRANSLATE of: rxn01786.seq check: 2034 from: 1 to: 684  
 MRAAKITRGFTSNPAGSVLVEFGNTRVMCTASVELGVPRFKRDSGEGWLTAEYAMLPAAT  
 AERNRRESMAGKVKGRTHEISRILGRSLRAAVDLSQLGENTIAIDCDVLQADGGTRTASI  
 TGAYVALADAIKVLQERGVVPGSPLLAPVAAVSVGLVDGNVCLDLPYEEDSRADVLDNVV  
 MTEHGEFVEIQGTGEETTFTRAQLNDMLDHAKEGCRELVAAQKAALGI

>RXN01876 TRANSLATE of: rxn01876.seq check: 6935 from: 1 to: 1851  
 MARPFYLATTVSPEGVHIRRHIRTGRVVTGVDDEVLTGEMADVIEQGGVGSSESVLHQAL  
 EQARSGHMRNIVETIQREQDEIIRDTRGMVMVQGGPGTGKTAVALHRVAYLLYTWRDQL  
 AKSGVLIIGPNKTFLEYISHVLPELGETGVVLSTVGELFPGIVPTGSEDLTREIKGSEE  
 MASILAEAVKAYQVLPKTIIVVSDGIEISIDEKTVAKSRTRARRARQSHNSARPIFREH  
 LVEQLAHQMAQTIGADPLGGKNLLSAADIDQLHDDLLDDAALQSVIDDFWPELRPQDVLH  
 DLLISEERINVAAGYDEETKSALLRGELDPWAPSDAALLDELALLIGLPDPEEAREKAE  
 AKWREQIDDAQEVLDVLSSSQSSDIDDVTEAEVLSAFDVIDAETLAQRQTVTDNRRTAER  
 AQADHKWAYGHVIVDEAQELSPMEWRMVFRSPSRWMTLVGDIAQTGWPAVDWAEESLW  
 PFVEKRFRHHELTVNYRTPAEIMSVANELLTQINPDIAPAIRESGREVVNLPLDADLS  
 AVMDSLREEDSQRTIAVISSRRHHESDFYLVDDIKGLEFDHVIVVDPAGIVEESPQGLQD  
 LYVAVTRATQSLTILGE

>RXN01912 TRANSLATE of: rxn01912.seq check: 1693 from: 1 to: 738  
 MRRFIFTERNGIYIIDLQQTLYIDQAFEFVKETVAHGGTVLFVGTGKKQAQEAQVEADR

VGMPYVNHRLGGMMLTNFQTVSKRLNRMKELQAMDAAENGYEGRTKREVLMLTRERTKLE  
 RVLGGIAEMTRVPSALWIIDTNKEHIAVAEAAHKLNI PVVAILDTNCDPDVDFVPVGNDD  
 AIRSTALLSRVISTAVEEGKKAREERQLAAAKDAAGDAKPEAAEAPAAAAEAEAPAAEAE  
 EAPAAE

> RXN01951 (1-561, translated) 187 residues  
 LLHYFDGEKR YILAPKGLTQ GTVIESGAAA DIKVGNNLPL RNIPTGTTIH NVELKPGAGA  
 KLARSAGASI QLLGKEGSYA VLRMPSSSEIR RVNIRCRATV GEVGNAEQIN IRWGKAGRMR  
 WKGWRPTVRG VVMNPVDHPH GGEGKTSYG RHPVSPWGQK EGRTRKPKRY SDDMIVRRRR  
 ANKNKKR

>RXN01966 TRANSLATE of: rxn01966.seq check: 3341 from: 1 to: 657  
 VSESENNTTPAVAARDRLVWVDLEMTGLDLKRHVIVEVAALVTDANLNLVLEGVDLVVH  
 ATEEEELAQMDDFVTNMHESGLTEQIRESAVTLKEAEDAVLALIEKHCDPAHPAPLAGNS  
 IATDRAFIREFHMPRLDEALHYRMVDVSSVKELARRWYPRVYKQPEKGLAHRALADIVES  
 IRELDYYRRSFFVAEPGPTSEQCADDAAVDRFAPYFD

>RXN01979 TRANSLATE of: rxn01979.seq check: 2139 from: 1 to: 1581  
 LGHDFRPDYRRIRDLLAGLAPNIPVLATTATANDRVVEDVRAQLEDGTGLFRGGIDRESL  
 YLSVNNLLNPTERPAWLATHLKELTGSGIIYCLTVSAAHDLADALNSVGWNVAAYTGRTE  
 AGERERLEHALINNEIKALVATSALGMGFDPDLGFVVHMGSPSPVSYQQIGRAGRGT  
 ARADVILLPGTEDKEIWEYFASVSFPREEVVRQLLAVLTDEAOSTVKLESQVDLSRSRL  
 QVLKVLDDVDGAVKRVRGVSTGQEWIYDAERYAGLEQARKIEQQSMVNYQNTTECRMLY  
 LRKELDDVEATTPCGRCDNCTGKTWGLDTDASITLKVDQQLQTPGVKIAPRKMWPTGISV  
 RGKIAGLEEGRALGRLNDIARGPALKALLDSGAYSDDPMMARIIEVLKNWDWTNRPANVV  
 ALGNTNFGSTEMI IQVAQSIAAVGRMNFAGVLPAPGAEEVMAQNSAYRVEALLKQWDWS  
 QGLQLVPGPILLVTDLIDTGWSVTVAGNGIAQRTSEKVLPPFALASRG

>RXN02038 TRANSLATE of: rxn02038.seq check: 6905 from: 1 to: 369  
 MSEPIQENVESNVADAADIAAATAATEEFTNTIGDAIATASEEETIEAAPVVLDGPIQT  
 VGRKRRAIVRVLVAGSGEFKCNRTLEEFYFPNKLHQQLIKAPLVLLDRLNQCNIASIK  
 GPK

>RXN02070 TRANSLATE of: rxn02070.seq check: 1536 from: 1 to: 1122  
 MTQVTESAVRSALSRVEDPEIGKPITELGMVKSVIDGSDVQVEVYLTIAACPMKTTIVT  
 NTEAALKDIDGVGVHVTTDVMSDEQRRALRVSLRGETSEPVIPFAQPGSTTRVYAVASG  
 KGGVGKSSMTVNLAALAKRGLSVGILDADIYGHSPGMLGSDQRPHQVDDMIMPQAAG  
 VKMISIAHFTEGNAPVVWRGPMHLHRAIQQFLTDVFWGDLIDILLDLPPGTGDIATVAQL  
 IPNAELLIVTTPQAAAAEVAERAGTISVQTNQKVAGVIENMSAMVLPDGTMTDVFGTGGG  
 QKIADRLTAVTGEVVKVIGSVPLDPNLRIGGDVGNPIAISEPHSPTAAAINIEIAEHLAHR  
 KVS LVGKTLGLGVK

>RXN02082 TRANSLATE of: rxn02082.seq check: 737 from: 1 to: 2910  
 MYLKSLTLKGFKSFASATTLKFEPGICAVVGPNGSGKSNVVDALAWVMGECSAKTLRGKK  
 MEDVIFAGAGDRKPLGRAEVTLTIDNSDGLPIEYTESVTRRMFRDGASEYEINGAKAR  
 LMDIQELLSDTGIGREMHIMVGQGLAEILES RPEERRAYIEEAAGVLKHHRRKEKAQRK  
 LQGMQVNLDRQLDLTHELAKQLKPLARQAEAAQRAATVQADLRDARFQIAGFEIVKLSEK  
 LETSTEREKMIREQAEAAQEQLLEATTQMEVEMELAEITPQAEAAQQLWFDLSSLAERV  
 SATMRIAADRASSGAADVYPYAGQDPDELLGRAETADKELELEMAVEMTTERLTSIQEEA  
 EDKAAQAREAREHLAQVRAISDRREGVVRLLASEESLRTQHTSAEEEAERLSEQLEEFI  
 GRILDVERERRLTDERKQGVDTDRAPLEELKQAKHEAEAAETRLEELRTRKSDLEKEVS  
 RLQSRIETLNQNRPRSDAADVVDYPQLATLIRPQRNVKALAAALGAHAEALAGEAAEGL  
 VEKLIDAGVARTIIVDGTQAGGAWRLDANI PAGASWLLDHVDLDPAIAGPVNRLADVVL  
 VDDPSLGRQAIEDDPRLRAVDRNGVLIGAGWIVGTETSTVEITAHIEEAQQLAAASAA  
 LDDIAGTFDGLHAADNTRVEVAARTAALRELDMTDRDSITRDLARLDKQHEAAESERVH  
 VGRLLHAAETRREELREQLEDIVDRLSRVEDEEDADEPSTTARDQANAELQQIRAMEMEAR  
 LAQRTAEERAGQQRGKDSLRRQAEHERQAKIRHEQAMEARRRRRTQLAAAVHNGARDVAE  
 RVSSVLAQAAIERDQHNRDKALLTSHLAKAKDAVSAARQHLNRLSDNAHSMELARSQAQV  
 RMEEAVAKITEQLGIPVAELLRDYTPDENFDEKQFQARLKQAEKDLAALGKVNPLALEEF  
 KALGRALRVP

>RXN02131 TRANSLATE of: rxn02131.seq check: 894 from: 1 to: 1671  
 VAFGDGPLIVQSDKTVLLEIDHPQAGEARIALAPFAELERAPEHIHTYRITPLALWNART  
 AGHDAEQVVDMLERFSRFPVPQALLIDIAETMSRYGRVRLHRHPAHGLILESSEPAIIVE  
 ISRHHKIKPMLGAQVDPETIVVHPSEGRGLKQELLKVGWPAEDLAGYVDGESHPIGLSTE  
 FEDWSLRDYQQMAADSFWEAGSGVVVLPAGAGKTMVGAASMARAAQATTLILVTNTVAGRQ  
 WKDELLRRTTLTEDEIGEYSGERKEIRPVTIATYQVVTRRTKGEYKALELFDSDRWGLII  
 YDEVHLLPAPVFRMTSDQLSRRRLGLTATLVREDGREGDVFSLIGPKRYDAPWKDLESQG  
 FIATADCVEIRSTMTDAERMVYATAESADRYRLAATAHTKVAVVRKLEEHAGKPTLIIG  
 AYLDQLEELGAEFNAPVIDGKTPNKKREALFDQFRSGSLSVLVVSKVANFSIDLPEASVA  
 IQVSGTFTGSRQEEAQLGRLLRPKHGSEAHFYSIVSRDTLDTEYAAHRQRFLAEQGYAY  
 RILDADDILFPLPKKEL

>RXN02293 TRANSLATE of: rxn02293.seq check: 2677 from: 1 to: 2388  
 MSSRIGNFLINRISTGLPVENIIPHLQEAFAAGPKNLVIQAPPGTGKTTLLPPLVANILC  
 NEGAGNATPTKVLVTAPRRVAVRAAARRLAQLDDSQLGTVGVFSVRGEHISGSHVQFMTP  
 GVLIRQLLNNPELPGIGAVIIDEVHERQLDSDLLGLMLAELSQRDDFSLIAMSATLDS  
 KFANLLDAQVLSVEAPIFPLDISYAPARAPRLNAKGVWDWDFLDHMAQKTHDAVTHSEHSA  
 LIFVPGVREIDRVMSTLKSGLHNNVFPLHGQLSPTEQDRALAPSQQQRIIVSTPVAESSL  
 TVPGVRIGVDSGLSRSPKRDARSMTGLITSSCAQASAGQAGRAGREGPGQIIRCYSEE  
 DFSHFPRFVTPEISSADLTQAALWLAQWGTSPADLPLLDQPPHAAWTAQQILRLIGALE  
 GDAITSLGHRSLTLPCLPQLSASLLRFGEQSakilAVVSENPOGDVEKQPPDKREVERLR  
 RLAPASVGKASAGQIVGAAPFQLIGRKIDNGEYLLASGTRARLMDSDLKDAEWISVAAIN  
 RSQNSAIIRAAARISEDDAIDIGVVEETRAIFVNGKVQARKVKAAGAIELSSTPTKPTP  
 AEASSETIATALAKGIDLFHFSDKAASLRDLRKFIHEHRGEPWPDIEADPHLWLSPEIE  
 ALSHGTRLNNDMPALQRLLPWPEATNFEFAPSHLSVPSGNQHRLDYSSGRPVIRVKL  
 QECFGLLESPQLCGIPVQFHLLSPAGRPLAVTDDLRSFWSGPYSQVRAEMRGYPKHPWP  
 EDPWTAPATARTKNRM

>RXN02357 TRANSLATE of: rxn02357.seq check: 4829 from: 1 to: 6300  
 MSSLIPIVHAAGSIQEGITEYLTTSFSLADKQVATELKRFLGHGDSGMFHGPYVRARLPYA  
 QAQEWENVLSWLPENFVPHYHQKAAFQRLSSLDNRGKDRRPDPTLVVVTGTGSGKTESFLY  
 PILDHALLRLKRQGGIKALLYPMNALANDQADRLARLIHNNPALKGVTAGITGEAKG  
 NRTQMGERELINDPQAMRVSPDILLTNYKMLDQLLLRSVDREMWQKSATSLOQLVLDEF  
 HTYDGAQGTDAVALLRLGLMLKSQQPANFLDDSAMHRPLGIITPVATSATLGSGDSGSP  
 MLDFAYTIFGERFPADAIVGETRLELDQWRAEIAQNFAPAVSEPRELPTVEDIEVLDLT  
 IATAQHEDDYAQLCFRVFCEKVLCEADLHAAISAYAAHDLTAAILQHAADSTPLSRDQ  
 DEVTALPELVLGATARIILGEVKAAEFISHALAAMAFVRAEYGVAAWGAARLPVGVETHLW  
 VREVSRIIDRALGVGDEQSMFRWSDDGPAEDANTQOWLPAICYCRSCGRSGWMVSLEQGTNI  
 PVLEEQKIRLNSFEQPHKQRALLDATSEQRAAIEQGRSVAGPRGVDGTSAVLWFHHSASNE  
 LSTRQPSPEEEQSGSSIAVLTHFGPEADDLQSAKQTCPSGCDVDSIRYIGSGISTLLSVSL  
 SNLFGMADLDSAEKKTILVFADSVQDAAHRAQYVQARSRAFAALRTYTRRAVGDNEVTLPSI  
 SRALMDNATSGRTRYELLPPDLTDLDIYKPYWHPDASKAERREASRNVHKRLSFDLALF  
 GQRADLPRSLALTGALSFAVDLPKGVALSAAAEALYAEVPTLDIEDENLRLRWVQGALE  
 LLRARGGINHEWFGAYLRTDGNPYMLNRRQARAEGIPGFVRGGAPEFPRVGSALSGSLRS  
 STGTTPLGSPRGYASWTSQVLGISTHDAATAITKLFDALSNRSILSSISTDSGGKIYCL  
 EAERIRIFSEDHPEVLECSVCHAQTGVTDHVRDFLDGAPCFSPSCGGVLHIEEVEDNYYR  
 RLYSAIEPRTVIAREHTSMLKKKDRLEQSFRRGEGSAKQSPDAPNVLVATPTLEMID  
 IGDLSVMLASLPTSVASYVQVRGRAGRLSGNSLVAVVRGRGVTLPRNLQPLSMIKGAI  
 TPPVAYLSASEILHRQFLAYVIDCLDTRAELPKLETAIDVFDNAAGKTPVALLKAQIHA  
 GLDPLLEEFVRTLNMQISIDNIFELRTWASGNSTDSLLALLETSQKEWMEERRSLTARRG  
 ELEKIFDKLDARNDADHEELKEEKRTAASLKAVKLQIRDLLGEFWIAALERYGLLPNFT  
 LVDDSVELNVAVTSFNPQEVFDTKNHAYSRGISAALFELAPGATFYAQGIAAKVDSIEI  
 GEHGSIAEQWRLCPVCSHSEILQPGVSTPGSCPTCGSPAFADKGQILEVVQMRKVSSAVE  
 KTRAAISDDREDRFRSTRFNQHVSVFVPPDGHGKSWYLDNGFGIEHLPKVELRWLNLGIGN  
 GQKRRLLGGFEVTSPLFNVCRHCHLDSEAGANSRWDHRPWCPHRYEQKEDTVSFALGRTL  
 KTQGVLMMLPEYFGSEADSMVVTSLIAAIKLGFRVVLGGDPDHLVDVTSVQVPTSGDGAL  
 DALLLHDQVPGGTGYLNQFADPTKVPPELISRWERVSRQCQYDETLACPECLLPYTRTD  
 TLLHTFRATAEKSLRAILLNSSRPEEITDLSAVPDWTFLEKRPENTLGSQLELRFVMLR  
 RALKNRHAKLVDRVNGSNSYVDIEMSSGVVRWRMSEQVDRGYTRPDFWFEPNGNYPTVAV  
 FTDGAAFHISSANYRLDGDIIQKRMKLALDPDNLIPWNITSLDLDRFSNPAAQGEPAWFS  
 PIGRQLSKANLILDPQSTALLAATPMDQLLAFLDNPAASSWKEFAHIAAAHMLGHNPPQKN

GDGIVGTFRNKISLRATMVNRELRARQLWLAPTTPEELEVDTWTAFNLNLANLMWLAPESV  
YVSTNGSPHKIDIVPAPAAPLVVEPELWAPILDGFTADEDEEAEGALQILAKEHALVPE  
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>RXN02370 TRANSLATE of: rxn02370.seq check: 1226 from: 1 to: 792  
MTPIYDDVDNDKLDPERILAESTVEPEEGPRMRARRRQESAADDIAAIAAAVVDIASE  
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SDHAPKPEDFAPVVEEVAETPVKTPARKAPRRNRPSSELSSGAPSSAPSTRNRRRAVRRL  
VEAPETVVEIAPEAAPEQVAEPQVEFDQPDNRRKRRRAVRVTAAPVEKKVASTSNARAPK  
KEPQAASTTNPGRRRRRATRRGPRS

>RXN02371 TRANSLATE of: rxn02371.seq check: 7071 from: 1 to: 315  
MYAIVKTGGKQYKVAEGDLVKVEKIEGEPGASVALTPVLLVDGADVTTAADKLASVSVNT  
EIVEHTKGPKIKILKYKNKTGYKKRQGHROPLTVLKVTGNQVSPR

>RXN02468 TRANSLATE of: rxn02468.seq check: 4275 from: 1 to: 1224  
VEITDALEALGINRTFAIQEYTLPIALDGHDFIGQARTGMGKTYGFGVPLLDVFDSDADV  
AETDGTPRALVIVPTRELAVQVGDDLQRAATNLPLKIFTFYGGTPYEEQIDALKVGVDDV  
VGTPGRLLDLHKGALS LDKVAILVLDEADEMLDLGFLPDIEKILRALTHQHQTMLFSAT  
MPGAILTLARSFLNKPVHIRAETSASATHKTTRQVVFQAHKMDKEAITAKILQSKDRGK  
TIIIFARTKRTAAQVAEDLASRGFSVSGSVHGDMPAREKSLNAFRTGKIDILVATDVAAR  
GIDVDDVTHVINYQTPDDPMTYVHRIGRTGRAGHNGTAVTLVGYDETLLKWTVIDNELELG  
QPNPPQWFSTSPELLETLDIPEGVTERVGPPTKVLGGTAPRPPRRTRK

>RXN02727 TRANSLATE of: rxn02727.seq check: 1998 from: 1 to: 912  
VULLPLLVPQLQVQPLQLPSLLTRQRCARKSKRSCAPNTASKLDDASKAAQKAQNDAS  
AQDQLQRAQADAKAARDEAEKAKAEAKSAASSSTTKAAAVGAVGAGTGAATGAANVDT  
HMQAQVLGLAQEMADRLTSEARSESMSMLDEAREAAEKQIEEANSTSNRTLEDARANAE  
KQIAEAQNRAATLVNEADAKAKNLVSEAEKKSATLAASTSRAEAQIRQAEDKANALQAD  
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PSGE

>RXN02764 TRANSLATE of: rxn02764.seq check: 4873 from: 1 to: 2784  
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VLERIRQGWEPSSMLVVATSKEAASRLRQEISESVAQMDYVSEGPLVRSVHSAFALIRD  
ASDDDVRLITGAEQDAVIRELLRGHADDGRGGWPQEQREGLRMVGFARQLRDFLLRAVER  
GVGPDELVELGERFERANWVAAGEFLREYKQVMKLSGAHSFSASELVTEALRGPEPSVKY  
RGVFIDDAQHLDPKSAELVSRFFPEAELAVVAGDPQQSVFRFRGANPDFLTKLSDHEVV  
LKGRRKASTSIVVAETESAHADLLADTVRRRAHLIDGRSWSEIAVIVRSAGMIAPIWRTLL  
AAGVPVHISPTDVVLAEQRIVAAMILGLRALTESLNAIELEDLLLGPIGGADPVTLRRL  
RGLRQAEMKMGQORRAIEVLRSLLAESDAEMLGLFTDRELNLLERVRSVLEAGREALAEH  
GSIEEVLWALWSATDLNSLSAISLRGGASGSQADRDLDAMMALFDAAGDYVERYPSAGV  
RSFILHISEQELPTGMRRERRGAIPEAVEVLTAHATTGREWKRVIVAEVQEGSWPSLGETG  
TLLGQEEFVDLVDEGIDPDIIISRSAERLAEERRLFYLATTRSTESLLVTAVNSPDSDEV  
REPSRFLELLSQPIVVLEGEESAIAEPEEIGHRLLSIPAMVAELRRVVNDPRDPRKQA  
ARQLSRLAEAGIPGANPAEWTNLRTPTSTDEELIKGAVSLSPSRIEQLLNCPRAVLDRLD  
SEEETPIAMLKGTLVHAFAEAVAGGVDAALAEKVTSAYMQLANVPSWSRESTEIAFRRI  
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IAAKMDGDHPQLFAYQLALSKGVLHGDK

>RXN02819 TRANSLATE of: rxn02819.seq check: 6309 from: 1 to: 1047  
KLQIGDVIAMPGRKRPVLAVVMTANQSRDPRPWVTTESGWSGRVDAESFTNPITIGHM  
RLPRQAIEEPRRNARRVQELFRREHFKRPNKMREFARVRPNEAVTKLRNAIRDHEAHHWP  
DREHLARTAERMIRKERDLAKLTGNVDKARETLGRTFERILSLLSEMDYVDYSNPDNPVI  
TDEGERLAKIHSEADLLVAQCLKRGIWNDLPAELAGVSMCTFENRRETGGEAQAVTEA  
MADSMNSVERIWGELVEDERRHRLPITRQPEAGFATAIHQWASGAPLGYCMAAAAENGAE  
LTPGDFVRWCRQVIDLLEQVAKTAYFDETTNRARQAIDAIRGVVAIGS

>RXN02826 TRANSLATE of: rxn02826.seq check: 160 from: 1 to: 435  
MAPKKKKKVTGLIKLQIQAGQANPAPPVGPALGAHGVNIMEFCKAYNAATENQRGNVVPP  
EITVYEDRSFDFKLKTPPAKLLLKAAGLQKGSVPHTQKVGKVSMAQVREIAETKKEDL

NARDIDAAAKIIAGTARSMGITVEG

>RXN02833 TRANSLATE of: rxn02833.seq check: 6083 from: 1 to: 783  
LLETWRQVVADLTTLTSSQQADSGFDPLTPTQRAYLNLTKEPIAIVDGYAVLSTPNAMAKNVI  
ENDLGDALTRVLSLRMGRSFSGLAVSVEPEQEIPETPAQQEFKYQPDAPVISSNKAPKQYE  
VGGRGEASTSDGWERHTSAPAPEPHAPAPIADREPELATPQRIPRETPAHNPNNREVSLNPK  
YTFESFVIGPFNRFANAAVAVAESPAAKAFNPLFISGGSGLGKTHLLHAVGNYAQELQPG  
PRIKYVSSEEHQRLHQLRAR

>RXN02943 TRANSLATE of: rxn02943.seq check: 6621 from: 1 to: 1668  
MSRISARTLAIALAGATAASLAVVPAATANPAGTAPVINEIYEGGGNSGSLFSNDFIELY  
NPTSGDISLDGWSVTYYAANGNSGGTTLNLTGNIPANGYYLIQQRAGSNNTGALPTPDATG  
NLAMGASQGSVALTDNSGLTADLVGFGGTSMFEGTAAAPETSNKLSVQRKEVGADSDNNS  
VDFETGAPTPTSSGGSAPVDPGEPETPVNPGETVSIAQIQGTGLATPLEGQTVTTEGIVT  
AVYAEAGGFNGYYIQTGSGGTAPKVGADSDGIFVYVGSNGSYPELGASVTVTGKATEHYE  
MTQLGNSSFTVSDTAFEPVTPLELDTVPTGDDIREAYEGMLLKPTGAHTVTNNYATNTFG  
EIALAPGNEPLYQATQMVAPGAEEAIAEAEVAKQITLDDGRSGNYTRGDSSTPMAWLQ  
DGGETIKSIRTGDQVEFQAPVIFDYRYDLWKFPPTTPTVTGNTASSDLPTWDDTRAAELA  
SINDVAGEFHIAFNVNLNYFTSLGEDEPGCSAYRDINNTPVTANNCNVRGAYTEEALEDQ  
QSKIVEAINRLDQDVL

>RXN02981 TRANSLATE of: rxn02981.seq check: 3652 from: 1 to: 366  
MARLAGVDLPRNKRMEVALTYIYGIGPARSKQLEETGISPDRLTDNLTDQIAALRDVI  
EGTWKVEGDLRRQVQADIRRKIEIGCYQGIRHRRGLPVRGQRTKTNARTRKGPKKTIAGK  
KK

>RXN03093 TRANSLATE of: rxn03093.seq check: 5261 from: 1 to: 1839  
VADTAGTTGSKKKYLVIVESATKAKKIQPYLGNDYIVEASVGHIRDLPARGAADIPAKYKK  
EPWARLGVDTDRGFAPLYVVSPPDKKKKVADLKAKLKLVDLLELLATDPDREGEAIAWHLE  
VLKPTVPVRRMVFNIEITKPAILAAAENTRELDENLVDAQETRRILDRLYGYEVSPVLWKK  
VMPRLSAGRVQSVATRVIVERERERMAFVSADYWDLSAEFNARENGKADSDNPSSFTARL  
STIDGNRVAQGRDFNDRGELTSEAVVVDKQRAEALAEALEGQEMAVVGVEEKPYTRRPYA  
PFMTSTLQQESGRKLHYTTSERTMRIAQRLYENGHITYMRTDSTSLSEQGMKAARDQALEL  
YGAEYVSPSPRTYDRKVKNSQEAHEAIRPAGETFATPGQLHGLDAEEFKLYELIWQRTV  
ASQMADAKGTSMKVTIGGTAKTGEKTEFNATGRTLTFPGFLRAYVETTRTADGRDVADNA  
EKRLPLLSEGDLKVLSEIADGHSTNPPARYTEASLVKKMEDLGIGRPSTYASIIKTIQD  
RGYVYSRGNALVPSWVAFAVVGLLEANFTSLVDYDFTSSMEDELNDIAAGREGRETEWLNQ  
FYFGRCSRSGSVHG

>RXN03139 TRANSLATE of: rxn03139.seq check: 8976 from: 1 to: 249  
MKQRNNAKRVRLQTRRPKNPLKAAGIEKVDYKDINTLRQFISDRHKIRSRRVTGLTPQ  
QREVATAVKNAREMALLPFTSR

>RXN03148 TRANSLATE of: rxn03148.seq check: 7950 from: 1 to: 366  
MVINFIIILFLMIAITSFFVASEFALVKIRRSRLQLEKENVKNAKLALHVTHHLDNYLSA  
SQLGITLTGLIIGWVGEGSVAALLEPVGKLPFSSAISSTISVALGFILVTVYRCGYWRT  
AS

>RXN03163 TRANSLATE of: rxn03163.seq check: 610 from: 1 to: 1497  
MAKTRVPAPPEKSVARVLPGLLGLPHLDRLFDYRISEDQHDDVQPGVVRVVRFGGRLVDAIV  
MSRTAQTSHEGKLMWLDREVISPVVYPPTAKLIEQLSDRYGGVRSDLIRSALPARHAGA  
EEADTSTSWESLGEVKEPDLSSWSAYQHGSFVDAVLGTTARASWQIAPGDDWALALAS  
LAVKVKDGGGALLVVPDQDRDLRLEAALRGLVAAKQITVLNSGLGPQARYRRFLSVLSG  
QGRLLIIGTRSAFAPVKDLKLAVILNDGDDNLVDPRAPYAHAREVLTRSSLEASSLIIA  
GHARTAETQLLVESGWMHNLIAPRDTIRTRMPRIQAVGDSDFQMERDPMARSARLPGIAF  
HAVRSALERDQPALIQVPRKGYVPTLACGNCRTPARCRHCNGPVGLPQGSSDLAGVPTCR  
WCGRPDSRFKQCNGSPKLRVVGLTERTAEELGRAFPVSRVITSGGNKVVDSVENRASI  
VVSTPGAEPFVANSPEPE

>RXN03166 TRANSLATE of: rxn03166.seq check: 5429 from: 1 to: 2235

MTTSETAPSKASLYELLEGVSLSDERTFRRRLSKARAPKALGAIKADIDKARLLIDEKSQ  
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HTQPRRLAARTVAERIADELGQDIGESVGYAIRFDDRVSSTSVKLMTDGILLAEMQRDR  
FLNAYDTIIIDEAHERSLNIDFILGYLRQLLPKRPDVKVIITSATIDPERFAEHFADASG  
KPAPIIEVSGRTFFVEIRYRPLEVLDGDKIIDTDPLDGLCSALEELMAEGDGDILCFFAG  
ERDIRDAMEAIEARRWKGVVEVTPLFGRLSNQEQRHVFSPHSGRRIVLSTNIAETSLTPVG  
IHYVVDTGATARISRYSVRTKVQRLPIENISQASANQRSGRGCRVADGIAIRLYSEDDFNS  
RPEFTDPEILRTNLASVILRMASRLGNDINFPFVQAPEQRSIRDGILLLLHELGAALTDDT  
QADGSPQLTQIGKDLANIPVDPRMARMLEANTLGCLHSMVIVSALTIQDVRERPLEFQ  
AQADQAHARFKDTSDFLGFLKLWEYIADQRNQSSGNSFRKQMKKEFLHYMRIREWDLV  
RQLEQIGQQLGWAKKEQVAGTASPDIIHQSLLTGLFSQIGSRDGESKEFTGARGTKFLVF  
PGSALTKKPPQFIMAGQLVETSRLWARDVAKIEPEWVEKAAGPLLKHQYSEPYWSSKRGG  
CHGAPQINALRCDNCCRQGSSEPHG

>RXN03175 TRANSLATE of: rxn03175.seq check: 2273 from: 1 to: 783  
VRASEKDTATALQPALDNGWHYIGAPAAAKGRAGVGILSRHELEDVNIGFGSFLDSGRYI  
EATIKDITLDVPVTVASLYLPSGSAGTDKQDEKYRFLDEFEGFLDQRAKERSHMVIGGDW  
NICHRRDLKNWKTNQKKSGLPDERAFMDSVFGTFPDEATQVAGAGDFFGAVDYEGTRR  
REATTDPAWFDVARRLQPEGDGPYTWWTYRGKAFDTGAGWRIDYQAATAAMLERASRWV  
DKAAAYDLRWSHSPNLVIYS

>RXN01389tr TRANSLATE of: rxn01389.seq check: 5202 from: 1 to: 684  
QDGDKLGRHGNKGVVGKILPQKDMFPLPDGTPVDIILNTHGVPRRMNIGQVLETHLGLW  
ASAGWSVDPEDPENAEVLKTLPLADLLEVPAGSLTATPVFDGASNEELAGLLANSRPNRDG  
DVMVNADGKATLIDGRSGEPYPYPVSIGYMYMLKLHHLVDEKIHARSTGPYSMITQQPLG  
GKAQFGGQRFGEVWAMQAYGAAYTLQELL